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/ECTORS FOR EXPRESSION O	F HML-2 POLYPEPTIDES					
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This collection of information is required by 37 CFR 1.51. The information is used by the public to file (and by the PTO to process) a provisional application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 8 hours to complete, including gathering, preparing, and submitting the complete provisional application to the PTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, Washington, D.C. 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Box Provisional Application, Assistant Commissioner for Patents, Washington, D.C.

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I hereby certify that this paper is being deposited in the United States Postal Service "Express Mail Post Office to Addressee", Express Mail Mailing Label No. EV 351353243Us under 37 CFR 1.10 on May 20, 2003, to Mail Stop Provisional Patent Application, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Nancy L. Swanson

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

STEPHEN F. HARDY et al.

Provisional Serial No::

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For:

VECTORS FOR EXPRESSION OF HML-2 POLYPEPTIDES

TRANSMITTAL LETTER

Mail Stop: Provisional Patent Application Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450

Sir:

Enclosed herewith are the following documents:

- 1. Provisional Application for Patent Cover Sheet
- 2. Specification (25 pages)
- 3. Drawings (7 sheets)
- Abstract (1 page)
- 5. Paper Sequence Listing (25 pages)

PATENT Atty. Docket No.PP-19482.002

- 6. Reference Listing (3 pages)
- 7. Check in the amount of \$160.00 covering filing fee.
- 8. Return postcard.

The Assistant Commissioner is hereby authorized to charge any additional fees (or credit any overpayment) associated with this communication and which may be required under 37 CFR 1.16 and 1.17 to Deposit Account No. 03-1664. This, however, is not authorization to pay the issue fee.

Respectfully submitted,

D17.

Marcella Lillis

Registration No.36,583

Date: May 20, 2003

polypeptide sequences are: SEQ ID 19 [HERV-K(C7)]; SEQ ID 20 [HERV-K10]; SEQ ID 21 ['ERVK6']; SEQ ID 73.

HML-2 env polypeptide is encoded by the fourth long ORF in a complete HML-2 genome. The translated polypeptide is proteolytically cleaved. Examples of env nucleotide sequences are: SEQ ID 22 [HERV-K(108)]; SEQ ID 23 [HERV-K(C7)]; SEQ ID 24 [HERV-K(II)]; SEQ ID 25 [HERV-K10]. Examples of env polypeptide sequences are: SEQ ID 26 [HERV-K(C7)]; SEQ ID 27 [HERV-K10]; SEQ ID 28 ['ERVK6'].

HML-2 cORF polypeptide is encoded by an ORF which shares the same 5' region and start codon as env. After around 87 codons, a splicing event removes env-coding sequences and the cORF-coding sequence continues in the reading frame +1 relative to that of env [19, 20]. cORF has also been called Rec [21]. Examples of cORF nucleotide sequences are: SEQ IDs 29 & 30 [HERV-K(108)]. An example of a cORF polypeptide sequence is SEQ ID 31.

The HML-2 polypeptide may alternatively be from a PCAP open-reading frame [22], such as PCAP1, PCAP2, PCAP3, PCAP4, PCAP4a or PCAP5 (SEQ IDs 32 to 37 herein). PCAP3 (SEQ IDs 34 & 46) and PCAP5 are preferred (SEQ ID 37).

The HML-2 polypeptide may alternatively be one of SEQ IDs 38 to 50 [22].

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Sequences encoding any HML-2 polypeptide expression product may be used in accordance with the invention (e.g. sequences encoding any one of SEQ IDs 5, 6, 7, 8, 9, 13, 14, 19, 20, 21, 26, 27, 28, 31-50, 69-74, 78 or 79).

The invention may also utilize sequences encoding polypeptides having at least a% identity to such wild-type HML-2 polypeptide sequences. The value of a may be 65 or more (e.g. 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.5, 99.9). These sequences include allelic variants, SNP variants, homologs, orthologs, paralogs, mutants etc. of the SEQ IDs listed in the previous paragraph.

The invention may also utilize sequences having at least b% identity to wild-type HML-2 nucleotide sequences. The value of b may be 65 or more (e.g. 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.5, 99.9). These sequences include allelic variants, SNP variants, homologs, orthologs, paralogs, mutants etc. of SEQ IDs 1, 2, 3, 4, 10, 11, 12, 15, 16, 17, 18, 22, 23, 24, 25, 29 and 30.

The invention may also utilize sequences comprising a fragment of at least c nucleotides of such wild-type HML-2 nucleotide sequences. The value of c may be 7 or more (e.g. 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 60, 70, 75, 80, 90, 100, 125, 150, 175, 200, 250, 300 or more). The fragment is preferably a proteolytic cleavage product

of a HML-2 polyprotein. The fragment preferably comprises a sequence encoding a T-cell or, preferably, a B-cell epitope from HML-2. T- and B-cell epitopes can be identified empirically (e.g. using the PEPSCAN method [23, 24] or similar methods), or they can be predicted e.g. using the Jameson-Wolf antigenic index [25], matrix-based approaches [26], TEPITOPE [27], neural networks [28], OptiMer & EpiMer [29, 30], ADEPT [31], Tsites [32], hydrophilicity [33], antigenic index [34] or the methods disclosed in reference 35 etc.

The invention may also utilize sequences encoding a polypeptide which comprises a fragment of at least d amino acids of wild-type HML-2 polypeptide sequences. The value of d may be 7 or more (e.g. 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 60, 70, 75, 80, 90, 100, 125, 150, 175, 200, 250, 300 or more). The fragment preferably comprises a T-cell or, preferably, a B-cell epitope from HML-2.

The invention may also utilize sequences comprising (i) a first sequence which is a wild-type HML-2 sequence or a sequence as disclosed above and (ii) a second non-HML-2 sequence. Examples of (ii) include sequences encoding: signal peptides, protease cleavage sites, epitopes, leader sequences, tags, fusion partners, N-terminal methionine, arbitrary sequences etc. Sequence (ii) will generally be located at the N- and/or C-terminus of (i).

Even though a nucleotide sequence may encode a HML-2 polypeptide which is found naturally, it may differ from the corresponding natural nucleotide sequence. For example, the nucleotide sequence may include mutations e.g. to take into account codon preference in a host of interest, or to add restriction sites or tag sequences.

THE SELECTABLE MARKER

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Vectors of the invention include a selectable marker.

The marker preferably functions in a microbial host (e.g. in a prokaryote, in a bacteria, in a yeast). The marker is preferably a prokaryotic selectable marker (e.g. transcribed under the control of a prokaryotic promoter).

For convenience, typical markers are antibiotic resistance genes.

FURTHER FEATURES OF NUCLEIC ACID VECTORS OF THE INVENTION

The vector of the invention is preferably an autonomously replicating episomal or extrachromosomal vector, such as a plasmid.

The vector of the invention preferably comprises an origin of replication. It is preferred that the origin of replication is active in prokaryotes but not in eukaryotes.

Preferred vectors thus include a prokaryotic marker for selection of the vector, a prokaryotic origin of replication, but a *eukaryotic* promoter for driving transcription of the

HML-2 coding sequence. The vectors will therefore (a) be amplified and selected in prokaryotic hosts without HML-2 polypeptide expression, but (b) be expressed in eukaryotic hosts without being amplified. This is ideal for nucleic acid immunization vectors.

The vector of the invention may comprise a eukaryotic transcriptional terminator sequence downstream of the HML2-coding sequence. This can enhance transcription levels. Where the HML2-coding sequence does not have its own, the vector of the invention preferably comprises a polyadenylation sequence. A preferred polyadenylation sequence is from bovine growth hormone.

The vector of the invention may comprise a multiple cloning site

In addition to sequences encoding a HML-2 polypeptide and a marker, the vector may comprise a second eukaryotic coding sequence. The vector may also comprise an IRES upstream of said second sequence in order to permit translation of a second eukaryotic polypeptide from the same transcript as the HML-2 polypeptide. Alternatively, the HML-2 polypeptide may be downstream of an IRES.

The vector of the invention may comprise unmethylated CpG motifs e.g. unmethylated DNA sequences which have in common a cytosine preceding a guanosine, flanked by two 5' purines and two 3' pyrimidines. In their unmethylated form these DNA motifs have been demonstrated to be potent stimulators of several types of immune cell.

PHARMACEUTICAL COMPOSITIONS

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The invention provides a pharmaceutical composition comprising a vector of the invention. The invention also provides the vectors' use as medicaments, and their use in the manufacture of medicaments for treating prostate cancer. The invention also provides a method for treating a patient with a prostate tumor, comprising administering to them a pharmaceutical composition of the invention. The patient is generally a human, preferably a human male, and more preferably an adult human male. Other diseases in which HERV-Ks have been implicated include testicular cancer [36], multiple sclerosis [37], and insulin-dependent diabetes mellitus (IDDM) [38], and the vectors may also be used against these diseases.

The invention also provides a method for raising an immune response, comprising administering an immunogenic dose of a vector of the invention to an animal (e.g. to a human).

Pharmaceutical compositions encompassed by the present invention include as active agent, the vectors of the invention in a therapeutically effective amount. An "effective amount" is an amount sufficient to effect beneficial or desired results, including clinical results. An effective amount can be administered in one or more administrations. For purposes of this invention, an effective amount is an amount that is sufficient to palliate, ameliorate, stabilize,

reverse, slow or delay the symptoms and/or progression of prostate cancer. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms.

The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. The effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01mg/kg to about 5 mg/kg, or about 0.01 mg/kg to about 50 mg/kg or about 0.05 mg/kg to about 10 mg/kg of the compositions of the present invention in the individual to which it is administered.

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The compositions can be used to treat cancer as well as metastases of primary cancer. In addition, the pharmaceutical compositions can be used in conjunction with conventional methods of cancer treatment, e.g. to sensitize tumors to radiation or conventional chemotherapy. The terms "treatment", "treating", "treat" and the like are used herein to generally refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete stabilization or cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any treatment of a disease in a mammal, particularly a human, and includes: (a) preventing the disease or symptom from occurring in a subject which may be predisposed to the disease or symptom but has not yet been diagnosed as having it; (b) inhibiting the disease symptom, i.e. causing regression of the disease or symptom.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be

prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g. mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in reference 39.

The composition is preferably sterile and/or pyrogen-free. It will typically be buffered at about pH 7.

Once formulated, the compositions contemplated by the invention can be (1) administered directly to the subject; or (2) delivered ex vivo, to cells derived from the subject (e.g. as in ex vivo gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g. subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Intramuscular injection is preferred.

Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art [e.g. ref. 40]. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the nucleic acid(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Targeted delivery

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Vectors of the invention may be delivered in a targeted way.

Receptor-mediated DNA delivery techniques are described in, for example, references 41 to 46. Therapeutic compositions containing a nucleic acid are administered in a range of about 100ng to about 200mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1µg to about 2 mg, about 5µg to about 500µg, and about 20µg to about 100µg of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g. for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy. Where greater expression is desired over a larger area of tissue, larger amounts of vector or the same amounts re-administered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of e.g.

a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect.

Vectors can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally references 47 to 50).

Viral-based vectors for delivery of a desired nucleic acid and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (e.g. references 51 to 61), alphavirus-based vectors (e.g. Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532); hybrids or chimeras of these viruses may also be used), poxvirus vectors (e.g. vaccinia, fowlpox, canarypox, modified vaccinia Ankara, etc.), adenovirus vectors, and adeno-associated virus (AAV) vectors (e.g. see refs. 62 to 67). Administration of DNA linked to killed adenovirus [68] can also be employed.

Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone [e.g. 68], ligand-linked DNA [69], eukaryotic cell delivery vehicles cells [e.g. refs. 70 to 74] and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in refs. 75 and 76. Liposomes (e.g. immunoliposomes) that can act as gene delivery vehicles are described in refs. 77 to 81. Additional approaches are described in refs. 82 & 83.

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in ref. 83. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation [e.g. refs. 84 & 85]. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun [86] or use of ionizing radiation for activating transferred genes [84 & 87].

Delivery DNA using PLG {poly(lactide-co-glycolide)} microparticles is a particularly preferred method e.g. by adsorption to the microparticles, which are optionally treated to have a negatively-charged surface (e.g. treated with SDS) or a positively-charged surface (e.g. treated with a cationic detergent, such as CTAB).

Vaccine compositions

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The pharmaceutical composition is preferably an immunogenic composition and is more preferably a vaccine composition. Such compositions can be used to raise antibodies in a mammal (e.g. a human) and/or to raise a cellular immune response (e.g. a response involving

T-cells such as CTLs, a response involving natural killer cells, a response involving macrophages etc.)

The invention provides the use of a vector of the invention in the manufacture of medicaments for preventing prostate cancer. The invention also provides a method for protecting a patient from prostate cancer, comprising administering to them a pharmaceutical composition of the invention.

Nucleic acid immunization is well known [e.g. refs. 88 to 94 etc.]

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The composition may additionally comprise an adjuvant. For example, the composition may comprise one or more of the following adjuvants: (1) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59™ [95; Chapter 10 in ref. 96], containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing MTP-PE) formulated into submicron particles using a microfluidizer, (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (2) saponin adjuvants, such as QS21 or StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes), which ISCOMS may be devoid of additional detergent [97]; (3) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (4) cytokines, such as interleukins (e.g. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12 etc.), interferons (e.g. gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc.; (5) monophosphoryl lipid A (MPL) or 3-O-deacylated MPL (3dMPL) [e.g. 98, 99]; (6) combinations of 3dMPL with, for example, QS21 and/or oil-in-water emulsions [e.g. 100, 101, 102]; (7) oligonucleotides comprising CpG motifs i.e. containing at least one CG dinucleotide, with 5-methylcytosine optionally being used in place of cytosine; (8) a polyoxyethylene ether or a polyoxyethylene ester [103]; (9) a polyoxyethylene sorbitan ester surfactant in combination with an octoxynol [104] or a polyoxyethylene alkyl ether or ester surfactant in combination with at least one additional non-ionic surfactant such as an octoxynol [105]; (10) an immunostimulatory oligonucleotide (e.g. a CpG oligonucleotide) and a saponin [106]; (11) an immunostimulant and a particle of metal salt [107]; (12) a saponin and an oil-inwater emulsion [108]; (13) a saponin (e.g. QS21) + 3dMPL + IL-12 (optionally + a sterol) [109]; (14) aluminium salts, preferably hydroxide or phosphate, but any other suitable salt may also be

used (e.g. hydroxyphosphate, oxyhydroxide, orthophosphate, sulphate etc. [chapters 8 & 9 of ref. 96]). Mixtures of different aluminium salts may also be used. The salt may take any suitable form (e.g. gel, crystalline, amorphous etc.); (15) chitosan; (16) cholera toxin or E.coli heat labile toxin, or detoxified mutants thereof [110]; (17) microparticles (i.e. a particle of ~100nm to ~150µm in diameter, more preferably ~200nm to ~30µm in diameter, and most preferably ~500nm to ~10µm in diameter) formed from materials that are biodegradable and non-toxic (e.g. a poly(a-hydroxy acid), a polyhydroxybutyric acid, a polyorthoester, a polyanhydride, a polycaprolactone etc., such as poly(lactide-co-glycolide) etc.) optionally treated to have a negatively-charged surface (e.g. with SDS) or a positively-charged surface (e.g. with a cationic detergent, such as CTAB); (18) monophosphoryl lipid A mimics, such as aminoalkyl glucosaminide phosphate derivatives e.g. RC-529 [111]; (19) polyphosphazene (PCPP); (20) a bioadhesive [112] such as esterified hyaluronic acid microspheres [113] or a mucoadhesive selected from the group consisting of cross-linked derivatives of poly(acrylic acid), polyvinyl alcohol, polyvinyl pyrollidone, polysaccharides and carboxymethylcellulose; (21) doublestranded RNA; or (22) other substances that act as immunostimulating agents to enhance the efficacy of the composition. Aluminium salts and/or MF59™ are preferred.

Vaccines of the invention may be prophylactic (i.e. to prevent disease) or therapeutic (i.e. to reduce or eliminate the symptoms of a disease).

SPECIFIC VECTORS OF THE INVENTION

Preferred vectors of the invention comprise: (i) a eukaryotic promoter; (ii) a sequence encoding a HML-2 polypeptide downstream of and operably linked to said promoter; (iii) a prokaryotic selectable marker; (iv) a prokaryotic origin of replication; and (v) a eukaryotic transcription terminator downstream of and operably linked to said sequence encoding a HML-2 polypeptide.

Particularly preferred vectors are shown in figures 2 to 8 (SEQ IDs 51 to 56 & 80).

VIRUS-LIKE PARTICLES

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HML-2 gag polypeptide has been found to assemble into virus-like particles (VLPs). This particulate form of the polypeptide has enhanced immunogenicity when compared to soluble polypeptide and is a preferred form of polypeptide for use in immunization and/or diagnosis.

Thus the invention provides a virus-like particle, comprising HML-2 gag polypeptide. The gag polypeptide may be myristoylated at its N-terminus.

The invention also provides a VLP of the invention for use as an immunogen or for use as a diagnostic antigen. The invention also provides the use of a VLP of the invention in the manufacture of a medicament for immunizing an animal.

The invention also provides a method of raising an immune response in an animal, comprising administering to the animal a VLP of the invention. The immune response may comprise a humoral immune response and/or a cellular immune response.

For raising an immune response, the VLP may be administered with or without an adjuvant as disclosed above. The immune response may treat or protect against cancer (e.g. prostate cancer).

The invention also provides a method for diagnosing cancer (e.g. prostate cancer) in a patient, comprising the step of contacting antibodies from the patient with VLPs of the invention. Similarly, the invention provides a method for diagnosing cancer (e.g. prostate cancer) in a patient, comprising the step of contacting anti-VLP antibodies with a patient sample.

The invention also provides a process for preparing VLPs of the invention, comprising the step of expressing gag polypeptide in a cell, and collecting VLPs from the cell. Expression may be achieved using a vector of the invention.

The VLP of the invention may or may not include packaged nucleic acid.

The gag polypeptide from which the VLPs are made can be from any suitable HML-2 virus (e.g. SEQ IDs 1-9, 69 & 78).

DEFINITIONS

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The term "comprising" means "including" as well as "consisting" e.g. a composition "comprising" X may consist exclusively of X or may include something additional e.g. X + Y.

The term "about" in relation to a numerical value x means, for example, $x\pm 10\%$.

The terms "neoplastic cells", "neoplasia", "tumor", "tumor cells", "cancer" and "cancer cells" (used interchangeably) refer to cells which exhibit relatively autonomous growth, so that they exhibit an aberrant growth phenotype characterized by a significant loss of control of cell proliferation (i.e. de-regulated cell division). Neoplastic cells can be malignant or benign and include prostate cancer derived tissue.

References to a percentage sequence identity between two nucleic acid sequences mean that, when aligned, that percentage of bases are the same in comparing the two sequences. This alignment and the percent homology or sequence identity can be determined using software programs known in the art, for example those described in section 7.7.18 of reference 114. A preferred alignment program is GCG Gap (Genetics Computer Group, Wisconsin, Suite Version 10.1), preferably using default parameters, which are as follows: open gap = 3; extend gap = 1.

References to a percentage sequence identity between two amino acid sequences means that, when aligned, that percentage of amino acids are the same in comparing the two sequences.

This alignment and the percent homology or sequence identity can be determined using software programs known in the art, for example those described in section 7.7.18 of reference 114. A preferred alignment is determined by the Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 2, BLOSUM matrix of 62. The Smith-Waterman homology search algorithm is taught in reference 115.

BRIEF DESCRIPTION OF DRAWINGS

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Figure 1 shows the pCMVkm2 vector, and Figures 2 to 8 show vectors formed by inserting sequences encoding HML-2 polypeptides into this vector.

Figure 9 shows the location of coding sequences in the HML2.HOM genome, with nucleotide numbering according to ref. 5.

Figure 10 is a western blot showing gag expression in transfected 293 cells. Lanes 1 to 4 are: (1) gag opt HML-2; (2) gag opt PCAV; (3) gag wt PCAV; (4) mock.

Figure 11 also shows western blots of transfected 293 cells. In Figure 11A the staining antibody was anti-HML-2, but in Figure 11B it was anti-PCAV. In both 11A and 11B lanes 1 to 4 are: (1) mock; (2) gag opt HML-2; (3) gag opt PCAV; (4) gag wt PCAV. The upper arrow shows the position of gag; the lower arrow shows the \(\beta\)-actin control.

Figure 12 shows electron microscopy of 293 cells expressing (12A) gag opt PCAV or (12B) gag opt HML-2.

MODES FOR CARRYING OUT THE INVENTION

Certain aspects of the present invention are described in greater detail in the non-limiting examples that follow. The examples are put forth so as to provide those of ordinary skill in the art with a disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all and only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Celsius, and pressure is at or near atmospheric.

Vectors for expressing HML-2 polypeptides

The basic pCMVkm2 vector is shown in figure 1. This vector has an immediate-early CMV enhancer/promoter and a bovine growth hormone transcription terminator, with a multiple cloning site in between. The vector also has a kanamycin resistance gene and a ColE1 origin of replication.

Sequences coding for HML-2 polypeptides being inserted between SalI and EcoRI in the multiple cloning site:

Figure	SEQ ID	HML-2 polypeptide
2	51	cORF
3	52	PCAP5
4	53	gag
5	54	gag
6	55	Prt
7	56	Pol

Except for the vector shown in figure 4 (SEQ ID 53), the inserted sequences were manipulated for codon preference, including addition of an optimal stop codon:

cORF manipulation:

Start with SEQ ID 57 (SEQ ID 43); manipulate to SEQ ID 58 (SEQ ID 67):

10	ATGAACCCATCAGAGATGCAAAGAAAAGCACCTCCGCGGAGACGGAGACATC ATGAACCCCAGCGAGATGCAGCGCAAGGCCCCCCCCGCCGCCGCCGCCACC	cORFwt_hml (1) corfopt_hml (1)
10	GCAATCGAGCACCGTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGA GCAACCGCGCCCCCTGACCCACAAGATGAACAAGATGGTGACCAGCGAGGA	cORFwt_hml (53) corfopt_hml (53)
15	ACAGATGAAGTTGCCATCCACCAAGAAGGCAGAGCCGCCAACTTGGGCACAA GCAGATGAAGCTGCCCAGCACCAAGAAGGCCGAGCCCCCCACCTGGGCCCAG	cORFwt_hml (105) corfopt_hml (105)
	CTAAAGAAGCTGACGCAGTTAGCTACAAAATATCTAGAGAACACAAAGGTGA CTGAAGAAGCTGACCCAGCTGGCCACCAAGTACCTGGAGAACACCAAGGTGA	cORFwt_hml (157) corfopt_hml (157)
20	CACAAACCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGT CCCAGACCCCGAGAGCATGCTGCTGGCCGCCCTGATGATCGTGAGCATGGT	cORFwt_hml (209) corfopt_hml (209)
25	GTCTGCAGGTGTACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGGAGCGCCGCGTGCCCAACAGCAGCGAGGAGACCGCCACCATCGAGAACGGC	cORFwt_hml (261) corfopt_hml (261)
23	CCATGA CCCGCTTAA	cORFwt_hml (313) corfopt_hml (313)

PCAP5 manipulation:

30 Start with SEQ ID 59 (SEQ ID 37); manipulate to SEQ ID 60 (SEQ ID 68):

	ATGAACCCATCGGAGATGCAAAGAAAAGCACCTCCGCGGAGACGAGACAT ATGAACCCCAGCGAGATGCAGCGCAAGGCCCCCCCCCC	
35	CGCAATCGAGCACCGTTGACTCACAAGATGAACAAAATGGTGACGTCAGAA CGCAACCGCGCCCCCTGACCCACAAGATGAACAAGATGGTGACCAGCGAG	pCAP5wt_hml (52) pcap5opt_hml (52)
	GAACAGATGAAGTTGCCATCCACCAAGAAGGCAGAGCCGCCAACTTGGGCA GAGCAGATGAAGCTGCCCAGCACCAAGAAGGCCGAGCCCCCACCTGGGCC	pCAP5wt_hml (103) pcap5opt_hml (103)
40	CAACTAAAGAAGCTGACGCAGTTAGCTACAAAATATCTAGAGAACACAAAG CAGCTGAAGAAGCTGACCCAGCTGGCCACCAAGTACCTGGAGAACACCAAG	pCAP5wt_hml (154) pcap5opt_hml (154)
45	GTGACACAAACCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCA GTGACCCAGACCCCCGAGAGCATGCTGCTGGCCGCCCTGATGATCGTGAGC	pCAP5wt_hml (205) pcap5opt_hml (205)
*1J	ATGGTGGTGTACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGC	pCAP5wt hml (256)

	PATENT
	PP-19482.002
	ATGGTGGTGTACCCCACCGCCCCAAGCGCCAGCGCCCCAGCCGCACCGGC pcap5opt_hml (256)
5	CATGATGACGATGGCGGTTTTGTCGAAAAGAAAGGGGGAAATGTGGGGAA pCAP5wt_hml (307) CACGACGACGACGGCGGCTTCGTGGAGAAGAAGCGCGGCAAGTGCGGCGAG pcap5opt_hml (307)
5	AAGCAAGAGAGATCAGATTGTTACTGTGTCTGTGTAGAAAGAA
10	AGGAGACTCCATTTTGTTCTGTACTAA pCAP5wt_hml (409) CGCCGCCTGCACTTCGTGCTGTACGCTTAA pcap5opt_hml (409)
	Gag manipulation:
	Start with SEQ ID 61 (SEQ ID 69); manipulate to SEQ ID 62 (SEQ ID 70):
15	ATGGGGCAAACTAAAAGTAAAATTAAAAGTAAATATGCCTCTTATCTCAGCT gagwt_hml (1) ATGGGCCAGACCAAGAGCAAGATCAAGAGCAAGTACGCCAGCTACCTGAGCT gagopt_hml (1)
	TTATTAAAATTCTTTTAAAAAGAGGGGGAGTTAAAGTATCTACAAAAAATCT gagwt_hml (53) TCATCAAGATCCTGCTGAAGCGCGGCGGCGTGAAGGTGAGCACCAAGAACCT gagopt_hml (53)
20	AATCAAGCTATTTCAAATAATAGAACAATTTTGCCCATGGTTTCCAGAACAA gagwt_hml (105) GATCAAGCTGTTCCAGATCATCGAGCAGTTCTGCCCCTGGTTCCCCGAGCAG gagopt_hml (105)
25	GGAACTTTAGATCTAAAAGATTGGAAAAGAATTGGTAAGGAACTAAAACAAG gagwt_hml (157) GGCACCCTGGACCTGAAGGACTGGAAGCGCATCGGCAAGGAGCTGAAGCAGG gagopt_hml (157)
23	CAGGTAGGAAGGGTAATATCATTCCACTTACAGTATGGAATGATTGGGCCAT gagwt_hml (209) CCGGCCGCAAGGGCAACATCATCCCCCTGACCGTGTGGAACGACTGGGCCAT gagopt_hml (209)
30	TATTAAAGCAGCTTTAGAACCATTTCAAACAGAAGAAGATAGCGTTTCAGTT gagwt_hml (261) CATCAAGGCCGCCCTGGAGCCCTTCCAGACCGAGGAGGACAGCGTGAGCGTG gagopt_hml (261)
	TCTGATGCCCCTGGAAGCTGTATAATAGATTGTAATGAAAACACAAGGAAAA gagwt_hml (313) AGCGACGCCCCGGCAGCTGCATCATCGACTGCAACGAGAACACCCGCAAGA gagopt_hml (313)
35	AATCCCAGAAAGAAACGGAAGGTTTACATTGCGAATATGTAGCAGAGCCGGT gagwt_hml (365) AGAGCCAGAAGGAGACCGAGGGCCTGCACTGCGAGTACGTGGCCGAGCCCGT gagopt_hml (365)
40	AATGGCTCAGTCAACGCAAAATGTTGACTATAATCAATTACAGGAGGTGATA gagwt_hml (417) GATGGCCCAGAGCACCCAGAACGTGGACTACAACCAGCTGCAGGAGGTGATC gagopt_hml (417)
40	TATCCTGAAACGTTAAAATTAGAAGGAAAAGGTCCAGAATTAGTGGGGCCCAT gagwt_hml (469) TACCCCGAGACCCTGAAGCTGGAGGGCCAAGGGCCCCGAGCTGGTGGGCCCCA gagopt_hml (469)
45	CAGAGTCTAAACCACGAGGCACAAGTCCTCTTCCAGCAGGTCAGGTGCCTGT gagwt_hml (521) GCGAGAGCAAGCCCCGCGGCCACCAGCCCCCTGCCCGCCGGCCAGGTGCCCGT gagopt_hml (521)
	AACATTACAACCTCAAAAGCAGGTTAAAGAAAATAAGACCCAACCGCCAGTA gagwt_hml (573) GACCCTGCAGCCCCAGAAGCAGGTGAAGGAGAACAAGACCCAGCCCCCCGTG gagopt_hml (573)
50	GCCTATCAATACTGGCCTCCGGCTGAACTTCAGTATCGGCCACCCCCAGAAA gagwt_hml (625) GCCTACCAGTACTGGCCCCCGCGAGCTGCAGTACCGCCCCCCCC
55	GTCAGTATGGATATCCAGGAATGCCCCCAGCACCACAGGGCCAGGGCGCCCATA gagwt_hml (677) GCCAGTACGGCTACCCCGGCATGCCCCCCGCCCCCCAGGGCCGCCCCCTA gagopt_hml (677)
<i>J</i> J	CCCTCAGCCGCCCACTAGGAGACTTAATCCTACGGCACCACCTAGTAGACAG gagwt_hml (729) CCCCCAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
60	GGTAGTAAATTACATGAAATTATTGATAAATCAAGAAAGGAAGG
	AGGCATGGCAATTCCCAGTAACGTTAGAACCGATGCCACCTGGAGAAGGAGC gagwt_hml (833) AGGCCTGGCAGTTCCCCGTGACCCTGGAGCCCATGCCCCCGGCGAGGGCGC gagopt_hml (833)
65	CCAAGAGGGAGAGCCTCCCACAGTTGAGGCCAGATACAAGTCTTTTTCGATA gagwt_hml (885) CCAGGAGGGCGAGCCCCCACCGTGGAGGCCCGCTACAAGAGCTTCAGCATC gagopt_hml (885)

	AAAAAGCTAAAAGATATGAAAGAGGGGGGTAAAACAGTATGGACCCAACTCCC AAGAAGCTGAAGGACATGAAGGAGGGCGTGAAGCAGTACGGCCCCAACAGCC	gagwt_hml (937) gagopt_hml (937)
5	$\tt CTTATATGAGGACATTATTAGATTCCATTGCTCATGGACATAGACTCATTCCCCTACATGCGCCACCGCCTGATCCCCTGCTGGACAGCATCGCCCACGGCCACCGCCTGATCCCCCTACCCCCCTGATCCCCCCCC$	
	${\tt TTATGATTGGGAGATTCTGGCAAAATCGTCTCTCTCACCCTCTCAATTTTTACTACGACTGGGAGATCCTGGCCAAGAGCAGCCTGAGCCCCAGCCAG$	
10	${\tt CAATTTAAGACTTGGTGGATTGATGGGGTACAAGAACAGGTCCGAAGAAATA}\\ {\tt CAGTTCAAGACCTGGTGGATCGACGGCGTGCAGGAGCAGGTGCGCCGCAACC}\\$	
15	${\tt GGGCTGCCAATCCTCCAGTTAACATAGATGCAGATCAACTATTAGGAATAGG} \\ {\tt GCGCCGCCAACCCCCCGTGAACATCGACGCCGACCAGCTGCTGGGCATCGG} \\$	gagwt_hml (1145) gagopt_hml (1145)
10	${\tt TCAAAATTGGAGTACTATTAGTCAACAAGCATTAATGCAAAATGAGGCCATT}\\ {\tt CCAGAACTGGAGCACCATCAGCCAGCAGGCCCTGATGCAGAACGAGGCCATC}\\$	
20	${\tt GAGCAAGTTAGAGCTATCTGCCTTAGAGCCTGGGAAAAAATCCAAGACCCAGGAGCAGGTGCGCGCCATCTGCCTGC$	gagwt_hml (1249) gagopt_hml (1249)
	${\tt GAAGTACCTGCCCCTCATTTAATACAGTAAGACAAGGTTCAAAAGAGCCCTAGCACCTGCCCCAGCTTCAACACCGTGCGCCAGGGCAAGGAGCCCTA}\\$	
25	${\tt TCCTGATTTTGTGGCAAGGCTCCAAGATGTTGCTCAAAAGTCAATTGCTGATCCCCGACTTCGTGGCCCGCCTGCAGGACGTGGCCCAGAAGAGCATCGCCGAC}$	
30	${\tt GAAAAAGCCCGTAAGGTCATAGTGGAGTTGATGGCATATGAAAACGCCAATCGAGAAGGCCCGCAAGGTGATCGTGGAGCTGATGGCCTACGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCGAGAACGCCAACCAACCGAGAACGCCAACCGAGAACGCCAACCAACCGAGAACGCCAACCAACCAACACAACA$	
	${\tt CTGAGTGTCAATCAGCCATTAAGCCATTAAAAGGAAAGG$	gagwt_hml (1457) gagopt_hml (1457)
35	AGATGTAATCTCAGAATATGTAAAAGCCTGTGATGGAATCGGAGGAGCTATGCGACGTGAAGGCCTGCGACGGCATCGGCGCGCCCATGCGACGCATCGGCGCGCGC	
	${\tt CATAAAGCTATGCTTATGGCTCAAGCAATAACAGGAGTTGTTTTAGGAGGACCACAAGGCCATGCTGATGGCCCAGGCCATCACCGGCGTGGTGCTGGGCGGCCCACCACCGGCCGTGGTGGTGGTGGGCGGCCCACCACCACCGGCGTGGTGCTGGGCGGCCCCACCACCACCACCACCACCACCACCACCACC$	<pre>gagwt_hml (1561) gagopt_hml (1561)</pre>
40	$\textbf{AAGTTAGAACATTTGGAAGAAAATGTTATAATTGTGGTCAAATTGGTCACTT} \\ \textbf{AGGTGCGCACCTTCGGCCGCAAGTGCTACAACTGCGGCCAGATCGGCCACCT} \\$	gagwt_hml (1613) gagopt_hml (1613)
45	AAAAAAGAATTGCCCAGTCTTAAATAAACAGAATATAACTATTCAAGCAACTGAAGAAGAACATGCCCCGTGCTGAACAAGCAGAACATCACCATCCAGGCCACC	gagwt_hml (1665) gagopt_hml (1665)
	lem:lem:lem:lem:lem:lem:lem:lem:lem:lem:	gagwt_hml (1717) gagopt_hml (1717)
50	${\tt ATTGGGCTAGTCAATGTCGTTCTAAATTTGATAAAATTGGGCAACCATTGTCACTGGGCCAGCCA$	gagwt_hml (1769) gagopt_hml (1769)
	${\tt GGGAAACGAGCAAAAGGGGCCAGCCTCAGGCCCCACAACAAACTGGGGCATTCCGGCAACGAGCAGCGCGGCCAGCCCCAGGCCCCCAGCAG$	gagwt_hml (1821) gagopt_hml (1821)
55	${\tt CCAATTCAGCCATTTGTTCCTCAGGGTTTTCAGGGACAACAACCCCCACTGTCCATCCA$	<pre>gagwt_hml (1873) gagopt_hml (1873)</pre>
60	$\tt CCCAAGTGTTTCAGGGAATAAGCCAGTTACCACAATACAACAATTGTCCCCC\\ GCCAGGTGTTCCAGGGCATCAGCCAGCTGCCCCAGTACAACAACTGCCCCCC\\$	
20	GCCACAAGCGGCAGTGCAGCAGTAG CCCCCAGGCCGCCGTGCAGCAGGCTTAA	<pre>gagwt_hml (1977) gagopt_hml (1977)</pre>

Prt manipulation:

65 Start with SEQ ID 63 (SEQ ID 71); manipulate to SEQ ID 64 (SEQ ID 72):

ATGTGGGCAACCATTGTCGGGAAACGAGCAAAGGGGCCAGCCTCAGGCCCCA Protwt_hml (1) ATGTGGGCCACCATCGTGGGCAAGCGCCCCAAGGGCCCCGCCAGCGCCCCA protopt_hml (1)

	CAACAAACTGGGGCATTCCCAATTCAGCCATTTGTTCCTCAGGGTTTTCAGG CCACCAACTGGGGCATCCCCAACAGCGCCATCTGCAGCAGCGGCTTCAGCGG	Protwt_hml (53) protopt_hml (53)
. 5	GACAACAACCCCCACTGTCCCAAGTGTTTCAGGGAATAAGCCAGTTACCACA CACCACCACCCCCACCGTGCCCAGCGTGAGCGGCAACAAGCCCGTGACCACC	Protwt_hml (105) protopt_hml (105)
10	ATACAACAATTGTCCCCCGCCACAAGCGGCAGTGCAGCAGTAGATTTATGTA ATCCAGCAGCTGAGCCCCGCCACCAGCGCAGCG	
10	CTATACAAGCAGTCTCTCTGCTTCCAGGGGAGCCCCCACAAAAAAACCCCCAC CCATCCAGGCCGTGAGCCTGCTGCCCGGCGAGCCCCCCAGAAGACCCCCAC	
15	AGGGGTATATGGACCCCTGCCTAAGGGGACTGTAGGACTAATCTTGGGACGA CGGCGTGTACGGCCCCCTGCCCAAGGGCACCGTGGGCCTGATCCTGGGCCGC	Protwt_hml (261) protopt_hml (261)
	TCAAGTCTAAATCTAAAAGGAGTTCAAATTCATACTAGTGTGGTTGATTCAG AGCAGCCTGAACCTGAAGGGCGTGCAGATCCACACCAGCGTGGTGGACAGCG	
20	ACTATAAAGGCGAAATTCAATTGGTTATTAGCTCTTCAATTCCTTGGAGTGC ACTACAAGGGCGAGATCCAGCTGGTGATCAGCAGCAGCATCCCCTGGAGCGC	
25	CAGTCCAAGAGACAGGATTGCTCAATTATTACTCCTGCCATACATTAAGGGT CAGCCCCGCGACCGCATCGCCCAGCTGCTGCTGCCCCTACATCAAGGGC	Protwt_hml (417) protopt_hml (417)
20	GGAAATAGTGAAATAAAAGAATAGGAGGGCTTGGAAGCACTGATCCAACAG GGCAACAGCGAGATCAAGCGCATCGGCGGCCTGGGCAGCACCGACCCCACCG	Protwt_hml (469) protopt_hml (469)
30	GAAAGGCTGCATATTGGGCAAGTCAGGTCTCAGAGAACAGACCTGTGTGTAA GCAAGGCCGCCTACTGGGCCAGCCAGGTGAGCGAGAACCGCCCCGTGTGCAA	
•	GGCCATTATTCAAGGAAAACAGTTTGAAGGGTTGGTAGACACTGGAGCAGAT GGCCATCATCCAGGGCAAGCAGTTCGAGGGCCTGGTGGACACCGGCGCCGAC	
35	GTCTCTATCATTGCTTTAAATCAGTGGCCAAAAAATTGGCCTAAACAAAAGG GTGAGCATCATCGCCCTGAACCAGTGGCCCAAGAACTGGCCCAAGCAGGA	
40	CTGTTACAGGACTTGTCGGCATAGGCACAGCCTCAGAAGTGTATCAAAGTAC CCGTGACCGGCCTGGTGGGCATCGGCACCGCCAGCGAGGTGTACCAGAGCAC	
	GGAGATTTTACATTGCTTAGGGCCAGATAATCAAGAAAGTACTGTTCAGCCA CGAGATCCTGCACTGCCTGGGCCCCGACAACCAGGAGAGCACCGTGCAGCCC	
45	ATGATTACTTCAATTCCTCTTAATCTGTGGGGTCGAGATTTATTACAACAAT ATGATCACCAGCATCCCCCTGAACCTGTGGGGCCCGGACCTGCTGCAGCAGT	
	GGGGTGCGGAAATCACCATGCCCGCTCCATCATATAGCCCCACGAGTCAAAA GGGGCGCCGAGATCACCATGCCCGCCCCCAGCTACAGCCCACCAGCCAG	
50	AATCATGACCAAGATGGGATATATACCAGGAAAGGGACTAGGGAAAAATGAA GATCATGACCAAGATGGGCTACATCCCCGGCAAGGGCCTGGGCAAGAACGAG	
55	GATGGCATTAAAATTCCAGTTGAGGCTAAAATAAATCAAGAAAGA	
	TAGGGAATCCTTGCTAG TCGGCAACCCCTGCGCTTAA	Protwt_hml (989) protopt_hml (989)
	Pol manipulation:	
60	Start with SEQ ID 65 (SEQ ID 73); manipulate to SEQ ID 66 (SEQ	ID 74):
	ATGAATAAATCAAGAAAGGAAGGAATAGGGAATCCTTGCTAGGGGCGGCCA ATGAACAAGAGCCGCAAGCGCCGCAACCGCGAGAGCCTGCTGGGCGCCCCA	
65	CTGTAGAGCCTCCTAAACCCATACCATTAACTTGGAAAAACAGAAAAACCAGT CCGTGGAGCCCCCAAGCCCATCCCCCTGACCTGGAAGACCGAGAAGCCCGT	
	GTGGGTAAATCAGTGGCCGCTACCAAAACAAAAACTGGAGGCTTTACATTTA	polwt_hml (105)

EU4FE189.05EQUS

			11-12-
	${\tt GTGGGTGAACCAGTGGCCCCTGCCCCAAGCAGCAGCTGGAGGCCCTGCACCTG}$	polopt_hml	(105)
5	${\tt TTAGCAAATGAACAGTTAGAAAAGGGTCATATTGAGCCTTCGTTCTCACCTTCTGGCCAACGAGCAGCTGGAGAAGGGCCACATCGAGCCCAGCTTCAGCCCCT}$	<pre>polwt_hml (polopt_hml</pre>	157) (157)
	${\tt GGAATTCTCCTGTGTTTGTAATTCAGAAGAAATCAGGCAAATGGCGTATGTT}\\ {\tt GGAACAGCCCCGTGTTCGTGATCCAGAAGAAGAGCGGCAAGTGGCGCATGCT}\\$	<pre>polwt_hml (polopt_hml</pre>	209) (209)
10	${\tt AACTGACTTAAGGGCTGTAAACGCCGTAATTCAACCCATGGGGCCTCTCCAAGACCGACC$	<pre>polwt_hml (polopt_hml</pre>	261) (261)
	${\tt CCCGGGTTGCCCTCTCCGGCCATGATCCCAAAAGATTGGCCTTTAATTATAACCCGGCCTGCCCAGCCCCGCCATGATCCCCAAGGACTGGCCCCTGATCATCA}$	<pre>polwt_hml (polopt_hml</pre>	(313) (313)
15	${\tt TTGATCTAAAGGATTGCTTTTTTACCATCCCTCTGGCAGGAGCAGGATTGCGATCGACCTGAAGGACTGCTTCTTCACCATCCCCTTGGCCGAGCAGGACTGCGAGCAGGACTGCGATCCCCTTGGCCGAGCAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGCAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGGACTGCGAGACTGCGAGGACTGCGAGACTGCAGAGACTGCAGACACACAC$	<pre>polwt_hml (polopt_hml</pre>	(365) (365)
20	AAAATTTGCCTTTACTATACCAGCCATAAATAATAAAGAACCAGCCACCAGG GAAGTTCGCCTTCACCATCCCGCCATCAACAACAAGGAGCCCGCCACCCGC	polwt_hml (polopt_hml	(417) (417)
	TTTCAGTGGAAAGTGTTACCTCAGGGAATGCTTAATAGTCCAACTATTTGTC TTCCAGTGGAAGGTGCTGCCCCAGGGCATGCTGAACAGCCCCACCATCTGCC	polwt_hml polopt_hml	(469) (469)
25	AGACTTTTGTAGGTCGAGCTCTTCAACCAGTTAGAGAAAAGTTTTCAGACTG AGACCTTCGTGGGCCGCGCCCTGCAGCCCGTGCGCGAGAAGTTCAGCGACTG	polwt_hml polopt_hml	(521) (521)
-	TTATATTATTCATTGTATTGATGATATTTTATGTGCTGCAGAAACGAAAGAT CTACATCACCTGCATCGACGACATCCTGTGCGCCGCGAGACCAAGGAC	<pre>polwt_hml polopt_hml</pre>	(573) (573)
30	AAATTAATTGACTGTTATACATTTCTGCAAGCAGAGGTTGCCAATGCTGGAC AAGCTGATCGACTGCTACACCTTCCTGCAGGCCGAGGTGGCCAACGCCGGCC	polopt_hml	(625)
35	TGGCAATAGCATCTGATAAGATCCAAACCTCTACTCCTTTTCATTATTTAGG TGGCCATCGCCAGCGACAAGATCCAGACCAGCACCCCCTTCCACTACCTGGG	polopt_hml	(677)
33	GATGCAGATAGAAAATAGAAAAATTAAGCCACAAAAAATAGAAATAAGAAAA CATGCAGATCGAGAACCGCAAGATCAAGCCCCAGAAGATCGAGATCCGCAAG	polopt_hml	(729)
40	GACACATTAAAAACACTAAATGATTTTCAAAAATTACTAGGAGATATTAATT GACACCCTGAAGACCCTGAACGACTTCCAGAAGCTGCTGGGCGACATCAACT	polopt_hml	(781)
	GGATTCGGCCAACTCTAGGCATTCCTACTTATGCCATGTCAAATTTGTTCTC GGATCCGCCCCACCTGGGCATCCCCACCTACGCCATGAGCAACCTGTTCAG	polopt_hml	(833)
45	TATCTTAAGAGGAGACTCAGACTTAAATAGTAAAAGAATGTTAACCCCAGAGCATCCTGCGCGGCGACAGCGACCTGAACAGCAAGCGCATGCTGACCCCCGAG	polopt_hml	(885)
50	GCAACAAAAGAAATTAAATTAGTGGAAGAAAAAATTCAGTCAG	polopt_hml	(937)
	ATAGAATAGATCCCTTAGCCCCACTCCAACTTTTGATTTTTGCCACTGCACA ACCGCATCGACCCCCTGGCCCCCTGCAGCTGGTCTTCGCCACCGCCCA	borobt_pur	(989)
55	TTCTCCAACAGGCATCATTATTCAAAATACTGATCTTGTGGAGTGGTCATTCCAGCCCCCACCGGCATCATCATCCAGAACACCGACCTGGTGGAGTGGAGCTTC	polopt_hml	(1041)
	CTTCCTCACAGTACAGTTAAGACTTTTACATTGTACTTGGATCAAATAGCTA CTGCCCCACAGCACCGTGAAGACCTTCACCCTGTACCTGGACCAGATCGCCA	bolobf_pmr	(1093)
60	CATTAATCGGTCAGACAAGATTACGAATAATAAAATTATGTGGGAATGACCCCCCTGATCGGCCAGACCCGCCTGCCCATCATCAAGCTGTGCGGCAACGACCC	: bolobf_pwr	(1145)
65	AGACAAAATAGTTGTCCCTTTAACCAAGGAACAAGTTAGACAAGCCTTTATCCGACAAGATCGTGGTGCCCCTGACCAAGGAGCAGGTGCGCCAGGCCTTCATC	: borobf_umr	(1197)
0 5	AATTCTGGTGCATGGAAGATTGGTCTTGCTAATTTTGTGGGAATTATTGATAAACAGCGGCGCCTGGAAGATCGGCCTGGCCAACTTCGTGGGCATCATCGACA	DOTOBE TUMT	(1249)
70	ATCATTACCCAAAAACAAAGATCTTCCAGTTCTTAAAATTGACTACTTGGAT ACCACTACCCCAAGACCAAGATCTTCCAGTTCCTGAAGCTGACCACCTGGAT	<pre>Polwt_hml Polopt_hml</pre>	(1301) (1301)

	TCTACCTAAAATTACCAGACGTGAACCTTTAGAAAATGCTCTAACAGTATTT CCTGCCCAAGATCACCCGCGGGGGCCCCTGGAGAACGCCCTGACCGTGTTC	polopt_hml (1353)
5	ACTGATGGTTCCAGCAATGGAAAAGCAGCTTACACAGGACCGAAAGAACGAGACCGACGGCAGCAACGGCAAGGCCGCC	polopt_hml (1405)
10	TAATCAAAACTCCATATCAATCGGCTCAAAGAGCAGAGTTGGTTG	polwt_hml (1457) polopt_hml (1457)
10	${\tt TACAGTGTTACAAGATTTTGACCAACCTATCAATATTATATCAGATTCTGCACCCGTGCTGCAGGACTTCGACCAGCCCATCAACATCATCAGCGACCAGCCCCCCCC$	polwt_hml (1509) polopt_hml (1509)
15	${\tt TATGTAGTACAGGCTACAAGGGATGTTGAGACAGCTCTAATTAAATATAGCA}\\ {\tt TACGTGGTGCAGGCCACCCGCGACGTGGAGACCGCCCTGATCAAGTACAGCA}\\$	polwt_hml (1561) polopt_hml (1561)
	${\tt TGGATGATCAGTTAAACCAGCTATTCAATTTATTACAACAAACTGTAAGAAA}\\ {\tt TGGACGACCAGCTGAACCAGCTGTTCAACCTGCTGCAGCAGACCGTGCGCAA}\\$	polwt_hml (1613) polopt_hml (1613)
20	eq:AAGAAATTTCCCATTTTATATTACACATATTCGAGCACACACA	polwt_hml (1665) polopt_hml (1665)
25	${\tt GGGCCTTTGACTAAAGCAAATGAACAAGCTGACTTACTGGT-ATCATCTGCA}\\ {\tt GGCCCCCTGACCAAGGCCAACGAGCAGGCCGACCTGCTGGTGAGCAGC-GCC}\\$	polwt_hml (1717) polopt_hml (1717)
25	$\tt CTCATAAAAGCACAAGAACTTCATGCTTTGACTCATGTAAATGCAGGATCTGATCAAGGCCCAGGAGCTGCACGCCCTGACCCACGTGAACGCCCGGCCCGGCCCCGGCCCCGGCCCGGCCGG$	polwt_hml (1768) polopt_hml (1768)
30	TAAAAAACAAATTTGATGTCACATGGAAACAGGCAAAAGATATTGTACAACA TGAAGAACAAGTTCGACGTGACCTGGAAGCAGGCCAAGGACATCGTGCAGCA	polwt_hml (1820) polopt_hml (1820)
	${\tt TTGCACCCAGTGTCAAGTCTTACACCTGCCCACTCAAGAGGCAGGAGTTAATCTGCACCCAGTGCCAGGTGCTGCACCTGCCCACCCA$	polwt_hml (1872) polopt_hml (1872)
35	${\tt CCCAGAGGTCTGTGTCCTAATGCATTATGGCAAATGGATGTCACGCATGTACCCCCGCGGCCTGTGCCCCAACGCCCTGTGGCAGATGGACGTGACCCACGTGC}$	polwt_hml (1924) polopt_hml (1924)
40	CTTCATTTGGAAGATTATCATATGTTCACGTAACAGTTGATACTTATTCACA CCAGCTTCGGCCGCCTGAGCTACGTGCACGTGACCGTGGACACCTACAGCCA	polwt_hml (1976) polopt_hml (1976)
40	TTTCATATGGGCAACTTGCCAAACAGGAGAAAGTACTTCCCATGTTAAAAAACTTCATCTGGGCCACCTGCCAGACCGGCGAGAGCACCAGCCACGTGAAGAAG	polwt_hml (2028) polopt_hml (2028)
45	CATTTATTGTCTTGTTTTGCTGTAATGGGAGTTCCAGAAAAAATCAAAACTG CACCTGCTGAGCTGCTTCGCCGTGATGGGCGTGCCCGAGAAGATCAAGACCG	polwt_hml (2080) polopt_hml (2080)
	ACAATGGACCAGGATATTGTAGTAAAGCTTTCCAAAAATTCTTAAGTCAGTG ACAACGGCCCCGGCTACTGCAGCAAGGCCTTCCAGAAGTTCCTGAGCCAGTG	polwt_hml (2132) polopt_hml (2132)
50	GAAAATTTCACATACAACAGGAATTCCTTATAATTCCCAAGGACAGGCCATA GAAGATCAGCCACACCACCGGCATCCCCTACAACAGCCAGGGCCAGGCCATC	polwt_hml (2184) polopt_hml (2184)
55	GTTGAAAGAACTAATAGAACACTCAAAACTCAATTAGTTAAACAAAAAGAAG GTGGAGCGCACCAACCGCACCCTGAAGACCCAGCTGGTGAAGCAGAAGGAGG	polwt_hml (2236) polopt_hml (2236)
33	GGGGAGACAGTAAGGAGTGTACCACTCCTCAGATGCAACTTAATCTAGCACT GCGGCGACAGCAAGGAGTGCACCACCCCCAGATGCAGCTGAACCTGGCCCT	polwt_hml (2288) polopt_hml (2288)
60	CTATACTTTAAATTTTTTAAACATTTATAGAAATCAGACTACTACTTCTGCA GTACACCCTGAACTTCCTGAACATCTACCGCAACCAGACCACCACCAGCGCC	polwt_hml (2340) polopt_hml (2340)
	GAACAACATCTTACTGGTAAAAAGAACAGCCCACATGAAGGAAAACTAATTT GAGCAGCACCTGACCGGCAAGAAGAACAGCCCCCCACGAGGGCAAGCTGATCT	polwt_hml (2392) polopt_hml (2392)
65	GGTGGAAAGATAATAAAAATAAGACATGGGAAATAGGGAAGGTGATAACGTG GGTGGAAGGACAACAAGAACAAGACCTGGGAGATCGGCAAGGTGATCACCTG	polwt_hml (2444) polopt_hml (2444)
70	GGGGAGAGGTTTTGCTTGTGTTTCACCAGGAGAAAATCAGCTTCCTGTTTGG GGGCCGCGGCTTCGCCTGCGTGAGCCCCGGCGAGAACCAGCTGCCCGTGTGG	polwt_hml (2496) polopt_hml (2496)

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	ATACCCACTAGACATTTGAAGTTCTACAATGAACCCATCAGAGATGCAAAGA ATCCCCACCCGCCACCTGAAGTTCTACAACGAGCCCATCCGCGACGCCAAGA	polwt_hml (2548) polopt_hml (2548)
	AAAGCACCTCCGCGGAGACGGAGACATCGCAATCGAGCACCGTTGACTCACA AGAGCACCAGCGCCGAGACCGAGACCAGCAGCAGCACCGTGGACAGCCA	polwt hml (2600)
	AGATGAACAAAATGGTGACGTCAGAAGAACAGATGAAGTTGCCATCCACCAA GGACGAGCAGAACGGCGACGTGCGCCGCCGACGAGGTGGCCATCCACCAG	polwt hml (2652)
10	GAAGGCAGAGCCGCCAACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCT GAGGGCCGCCGCCAACCTGGGCACCACCAAGGAGGCCGACGCCGTGAGCT	polwt hml (2704)
	ACAAAATATCTAGAGAACACAAAGGTGACACAAACCCCAGAGAGTATGCTGC ACAAGATCAGCCGCGAGCACAAGGGCGACACCCAACCCCCGGGAGTACGCCGC	polwt hml (2756)
15	TTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGG CTGCAGCCTGGACGACTGCATCAACGGCGGCAAGAGCCCCTACGCCTGCCGC	polwt hml (2808)
20	AGCAGCTGCAGCGCTTAA AGCAGCTGCAGCGCTTAA	polwt_hml (2860) polopt_hml (2860)

Env manipulation:

Start with SEQ ID 81 (SEQ ID 83); manipulate to SEQ ID 82:

25	envwt_HML2 envopt_HML2	ATGAACCCAAGCGAGATGCAAAGAAAAGCACCTCCGCGGAGACGGAGACATCGCAATCGA ATGAACCCCAGCGAGATGCAGCGCAAGGCCCCCCCCCGCCGCCGCCGCCACCGCAACCGC
	envwt_HML2 envopt_HML2	GCACCGTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAACAGATGAAGTTGCCA GCCCCCTGACCCACAAGATGAACAAGATGGTGACCAGCGAGGAGCAGATGAAGCTGCCC
30	envwt_HML2 envopt_HML2	TCCACCAAGAAGGCAGAGCCGCCAACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCT AGCACCAAGAAGGCCGAGCCCCCACCTGGGCCCAGCTGAAGAAGCTGACCCAGCTGGCC
	envwt_HML2 envopt_HML2	ACAAAATATCTAGAGAACACAAAGGTGACACAAACCCCAGAGAGTATGCTGCTTGCAGCC ACCAAGTACCTGGAGAACACCAAGGTGACCCAGACCCCCGAGAGCATGCTGCTGGCCGCC
35	envwt_HML2 envopt_HML2	TTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCAGCTAAC CTGATGATCGTGAGCATGGTGGTGAGCCTGCCCATGCCCGCCGGCGCCGCCGCCGCCAAC
40	envwt_HML2 envopt_HML2	TATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGG
·	envwt_HML2 envopt_HML2	AATCCTACAGAAGTATATGTTAATGATAGTGTATGGGTACCTGGCCCCATAGATGATCGC AACCCCACCGAGGTGTACGTGAACGACAGCGTGTGGGTGCCCGGCCCCATCGACGACCGC
45	envwt_HML2 envopt_HML2	TGCCCTGCCAAACCTGAGGAAGAAGGGATGATGATAAATATTTCCATTGGGTATCATTAT TGCCCCGCCAAGCCCGAGGAGGAGGGCATGATGATCAACATCAGCATCGGCTACCACTAC
	envwt_HML2 envopt_HML2	CCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAATGCCTGCAGTCCAAAATTGGTTG CCCCCCATCTGCCTGGGCCGCCCCCGGCTGCCTGATGCCCGCCGTGCAGAACTGGCTG
50	envwt_HML2 envopt_HML2	GTAGAAGTACCTACTGTCAGTCCCATCTGTAGATTCACTTATCACATGGTAAGCGGGATG GTGGAGGTGCCCACCGTGAGCCCCATCTGCCGCTTCACCTACCACATGGTGAGCGGCATG
55	envwt_HML2 envopt_HML2	TCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTT AGCCTGCGCCCCCGCGTGAACTACCTGCAGGACTTCAGCTACCAGCGCAGCCTGAAGTTC
	envwt_HML2 envopt_HML2	AGACCTAAAGGGAAACCTTGCCCCAAGGAAATTCCCAAAGAATCAAAAAATACAGAAGTT CGCCCCAAGGGCAAGCCCTGCCCCAAGGAGATCCCCAAGGAGAGCAAGAACACCGAGGTG
60	envwt_HML2 envopt_HML2	TTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATGAATTCGGA CTGGTGTGGGAGGAGTGCGTGGCCAACAGCGCCGTGATCCTGCAGAACAACGAGTTCGGC

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	envwt_HML2 envopt_HML2	ACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAG ACCATCATCGACTGGGCCCCCCGCGGCCAGTTCTACCACAACTGCAGCGGCCAGACCCAG
5	envwt_HML2 envopt_HML2	TCGTGTCCAAGTGCACAAGTGAGTCCAGCTGTTGATAGCGACTTAACAGAAAGTTTAGAC AGCTGCCCCAGCGCCCAGGTGAGCCCCGCCGTGGACAGCCGACCTGACCGAGAGCCTGGAC
10	envwt_HML2 envopt_HML2	AAACATAAGCATAAAAATTGCAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAGGAATC AAGCACAAGCACAAGAAGCTGCAGAGCTTCTACCCCTGGGAGTGGGGGCGAGAAGGGCATC
	envwt_HML2 envopt_HML2	TCTACCCCAAGACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGG AGCACCCCCGCCCCAAGATCGTGAGCCCCGTGAGCGCCCCGAGCACCCCGAGCTGTGG
15	envwt_HML2 envopt_HML2	AGGCTTACTGTGGCTTCACACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACA CGCCTGACCGTGGCCAGCCACCACATCCGCATCTGGAGCGGCAACCAGACCCTGGAGACC
	envwt_HML2 envopt_HML2	AGAGATCGTAAGCCATTTTATACTATTGACCTGAATTCCAGTCTAACAGTTCCTTTACAA CGCGACCGCAAGCCCTTCTACACCATCGACCTGAACAGCAGCCTGACCGTGCCCCTGCAG
20	envwt_HML2 envopt_HML2	AGTTGCGTAAAGCCCCCTTATATGCTAGTTGTAGGAAATATAGTTATTAAACCAGACTCC AGCTGCGTGAAGCCCCCCTACATGCTGGTGGTGGGCAACATCGTGATCAAGCCCGACAGC
	envwt_HML2 envopt_HML2	CAGACTATAACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGG CAGACCATCACCTGCGAGAACTGCCGCCTGCTGACCTGCATCGACAGCACCTTCAACTGG
25	envwt_HML2 envopt_HML2	CAACACCGTATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGAC CAGCACCGCATCCTGCTGGTGCGCCCCGCGAGGGCGTGTGGATCCCCGTGAGCATGGAC
30	envwt_HML2 envopt_HML2	CGACCGTGGGAGGCCTCGCCATCCGTCCATATTTTGACTGAAGTATTAAAAGGTGTTTTA CGCCCTGGGAGGCCAGCCCCAGCGTGCACATCCTGACCGAGGTGCTGAAGGGCGTGCTG
	envwt_HML2 envopt_HML2	AATAGATCCAAAAGATTCATTTTACTTTAATTGCAGTGATTATGGGATTAATTGCAGTC AACCGCAGCAAGCGCTTCATCTTCACCCTGATCGCCGTGATCATGGGCCTGATCGCCGTG
35	envwt_HML2 envopt_HML2	ACAGCTACGGCTGCTGTAGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCAG
40	envwt_HML2 envopt_HML2	GTTAATGATTGGCAAAAAAATTCTACAAGATTGTGGAATTCACAATCTAGTATTGATCAA GTGAACGACTGGCAGAAGAACAGCACCCGCCTGTGGAACAGCCAGAGCAGCATCGACCAG
	envwt_HML2 envopt_HML2	AAATTGGCAAATCAAATTAATGATCTTAGACAAACTGTCATTTGGATGGGAGACAGAC
45	envwt_HML2 envopt_HML2	ATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTCAGATTTTTGTATT ATGAGCCTGGAGCACCGCTTCCAGCTGCAGTGCGACTGGAACACCAGCGACTTCTGCATC
	envwt_HML2 envopt_HML2	ACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAG ACCCCCAGATCTACAACGAGAGCGAGCACCACTGGGACATGGTGCGCCGCCACCTGCAG
50	envwt_HML2 envopt_HML2	GGAAGAGAAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAACAAATTTTCGAAGCA GGCCGCGAGGACAACCTGACCCTGGACATCAGCAAGCTGAAGGAGCAGATCTTCGAGGCC
55	envwt_HML2 envopt_HML2	TCAAAAGCCCATTTAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGC AGCAAGGCCCACCTGAACCTGGTGCCCGGCACCGAGGCCATCGCCGGCGTGGCCGACGGC
	envwt_HML2 envopt_HML2	CTCGCAAATCTTAACCCTGTCACTTGGGTTAAGACCATTGGAAGTACTACGATTATAAAT CTGGCCAACCTGAACCCCGTGACCTGGGTGAAGACCATCGGCAGCACCATCATCAAC
60	envwt_HML2	CTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTAGTCTGCAGGTGTACCCAACAG CTGATCCTGATCCTGGTGTGCCTGTTCTGCCTGCTGCTGGTGTGCCGCTGCACCCAGCAG

envwt_HML2 envopt HML2 CTCCGAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCGAAA CTGCGCCGCGACAGCGACCACCGCGAGCGCCCCATGATGACCATGGCCGTGCTGAGCAAG

envwt_HML2 envopt_HML2

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AGAAAAGGGGGAAATGTGGGGAAAAGCAAGAGAGATCAGATTGTTACTGTGTCTGTGGCCTAA CGCAAGGGCGGCAACGTGGGCAAGAGCAAGCGCGACCAGATCGTGACCGTGAGCGTGGCCTAA

IN VITRO EXPRESSION OF GAG SEQUENCES

Three different gag-encoding sequences were cloned into the pCMVKm2 vector:

- (1) gag opt HML-2 (SEQ ID 54, including SEQ ID 62 and encoding SEQ ID 70 Fig. 5).
- (2) gag opt PCAV (SEQ ID 80, including SEQ ID 77 and encoding SEQ ID 79 Fig. 8).
 - (3) gag wt PCAV (SEQ ID 53, including SEQ ID 76 and encoding SEQ ID 78 Fig. 4).

The vectors were used to transfect 293 cells in duplicate in 6-well plates, using the polyamine reagent *TransIt*TM *LT-1* (PanVera Corp, Madison WI) plus 2 µg DNA.

Cells were lysed after 48 hours and analyzed by western blot using pooled mouse antibody against HML2-gag as the primary antibody (1:400), and goat anti-mouse HRP as the secondary antibody (1:20000). Figure 10 shows that 'gag opt PCAV' (lane 2) expressed much more efficiently than 'gag wt PCAV' (lane 3). Lane 1 ('gag opt HML-2') is more strongly stained than lane 2 ('gag opt PCAV'), but this could be due to the fact that the primary antibody was raised against the homologous HML-2 protein, rather than reflecting a difference in expression efficiency. To address this question, antibodies were also raised against the PCAV product and were used for Western blotting. Figure 11A shows results using the anti-HML2 as the primary antibody (1:500), and Figure 11B shows the results with anti-PCAV (1:500). Each antibody stains the homologous protein more strongly than the heterologous protein.

NUCLEIC ACID IMMUNIZATION

Vectors of the invention are purified from bacteria and used to immunize mice.

T CELL RESPONSES TO PCAV GAG

CB6F1 mice were intramuscularly immunized with pCMVKm2 vectors encoding PCAV gag (Figures 4 & 8) and induction of gag-specific CD4+ and CD8+ cells were measured.

Mice received four injections of 50µg plasmid at week 0, 2, 4 and 6. These plasmids included the wild type gag sequence (SEQ ID 76). Mice were then split into two separate groups for further work.

The first group of three mice received a further 50µg of plasmid at 25 weeks, but this plasmid included the optimized gag sequence (SEQ ID 77). Eleven days later spleens were harvested and pooled and a single cell suspension was prepared for culture. Spleen cells (1 x 10⁶ per culture) were cultured overnight at 37°C in the absence ("unstimulated") or presence

("stimulated") of 1 x 10⁷ plaque-forming units (pfu) of a recombinant vaccinia which contains the PCAV gag sequence ("rVV-gag", produced by homologous recombination of cloning vector pSC11 [116], followed by plaque purification of recombinant rVVgag). Duplicate stimulated and unstimulated cultures were prepared. The following day Brefeldin A was added to block cytokine secretion and cultures were continued for 2 hours. Cultures were then harvested and stained with fluorescently-labeled monoclonal antibodies for cell surface CD8 and intracellular gamma interferon (IFN-?). Stained samples were analyzed by flow cytometry and the fraction of CD8+ cells that stained positively for intracellular IFN-? was determined. Results were as follows:

Culture condition	Culture #1	Culture #2	Average
Unstimulated	0.10	0.14	0.12
Stimulated	1.51	1.27	1.39
	· · · · · · · · · · · · · · · · · · ·	Difference	1.27

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An average of 1.27% of the pooled splenic CD8+ cells synthesized IFN-? in response to stimulation with rVV-gag. This demonstrates that the DNA immunization induced CD8+ T cells that specifically recognized and responded to PCAV gag.

The second group of four mice received a further 50µg of plasmid at 28 weeks, but this plasmid included the optimized gag sequence (SEQ ID 77). Twelve days later spleens were harvested. As a specificity control, a spleen was also obtained from a CB6F1 mouse that had been vaccinated with a pCMV-KM2 vector encoding HML2 env.

Single cell suspensions from individual spleens were prepared for culture. Spleen cells (1 x 10⁶ per culture) were cultured overnight at 37°C in the absence of stimulation or in the presence of 1 x 10⁷ pfu rVV-gag. As a specificity control, additional cultures contained another recombinant vaccinia virus, rVV-HIVgp160env.SF162 ("rVV-HIVenv" – contains full-length env gene from SF162 isolate of HIV-1), which was not expected to cross-react with either gag or env from PCAV.

Duplicate cultures were prepared for each condition. The following day Brefeldin A was added to block cytokine secretion and anti-CD28 antibody was added to co-stimulate CD4 T cells. Cultures were continued for 2 hours and then harvested and stained with fluorescently-labeled monoclonal antibodies for cell surface CD8 and CD4 and intracellular IFN-? Stained samples were analyzed by flow cytometry and the fractions of CD8+CD4- and CD4+8- T cells that stained positively for intracellular IFN-? were determined. Results are shown in the following table, expressed as the % of stained cells in response to stimulation by either PCAV gag or HIV env during spleen culture, after subtraction of the average value seen with cells which were not stimulated during spleen culture:

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Spleen culture	Vector administered at 28 weeks						
stimulation	PCAV gag	PCAV gag	PCAV gag	PCAV gag	PCAV env		
CD8							
PCAV gag	1.32	1.88	3.00	2.09	0.13		
HIV env	0.04	0.12	-0.02	0.23	0.05		
CD4					•		
PCAV gag	0.26	0.17	0.40	0.22	-0.01		
HIV env	0.01	-0.02	-0.03	0.01	-0.02		

For the 4 mice that had been vaccinated with a vector encoding PCAV gag, therefore, the rVV-gag vector stimulated 1.32% to 3.00% of CD8+ T cells to produce IFN-?. However, there were few CD8+ T cells (<0.23%) that responded to the irrelevant rVV-HIVgp160env vector. The CD8+ T cell response is thus specific to PCAV gag. Furthermore, the control mouse that was immunized with PCAV env had very few CD8+ T cells (0.13%) which responded to the vaccinia stimulation.

Similarly, vaccination with PCAV gag, but not with PCAV env, induced CD4+ T cells specific for PCAV gag (0.17% to 0.40%).

DNA immunization with vectors encoding PCAV gag thus induces CD8+ and CD4+ T cells that specifically recognize and respond to the PCAV gag antigen.

VIRUS-LIKE PARTICLES

293 cells were fixed 48 hours after transient transfection with pCMV-gag, either from HML-2 or from PCAV, and inspected by electron microscopy (Figure 12). VLPs were produced in both cases, but these were mainly intracellular for PCAV and mainly secreted for HML-2.

The assembly of viable VLPs from PCAV and HML-2 indicates that the gag protein has retained its essential activity even though the endogenous virus is "dormant" and might thus be expected to be subject to mutational inactivation.

The above description of preferred embodiments of the invention has been presented by way of illustration and example for purposes of clarity and understanding. It is not intended to be exhaustive or to limit the invention to the precise forms disclosed. It will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that many changes and modifications may be made thereto without departing from the spirit of the invention. It is intended that the scope of the invention be defined by the appended claims and their equivalents.

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SEQUENCE LISTING INDEX

SEQ ID	DESCRIPTION		
1-9	Gag sequences		
10-14	Prt sequences		
15-21	Pol sequences		
22-28	Env sequences		
29-31	cORF sequences		
32-37	PCAP sequences		
38-50	Splice variants A-M sequences		
51	pCMVKm2.cORFopt HML-2 (Figure 2)		
52	pCMVKm2.pCAP5opt HML-2 (Figure 3)		
53	pCMVKm2.gag wt PĆAV (Figure 4)		
54	pCMVKm2.gagopt HML-2 (Figure 5)		
55	pCMVKm2.Protopt HML-2 (Figure 6)		
56	pCMVKm2.Polopt HML-2 (Figure 7)		
57-66	Nucleotide sequences pre- and post-manipulation		
67	Manipulated cORF		
68	Manipulated PCAP5		
69 & 70	Gag — pre- and post-manipulation		
71 & 72	Prt — pre- and post-manipulation		
73 & 74	Pol — pre- and post-manipulation		
75	PCAV, from the beginning of its first 5' LTR to the end of its fragmented 3' LTR		
76 & 77	PCAV Gag nucleotide sequences — pre-and post manipulation		
78 & 79	PCAV Gag amino acid sequences — pre-and post manipulation		
80	pCMVKm2.gagopt PCAV (Figure 8)		
81	Wild-type env from HML-2		
82	Optimized env from HML-2		
83	Amino acid sequence encoded by SEQ IDs 81 & 82		

NB:

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- SEQ IDs 1 to 9 disclosed in reference 1 as SEQ IDs 85, 91, 97, 102, 92, 98, 103, 104 & 146
- SEQ IDs 10 to 14 disclosed in reference 1 as SEQ IDs 86, 99, 105, 106 & 147
 - SEQ IDs 15 to 21 disclosed in reference 1 as SEQ IDs 87, 93, 100, 107, 94, 108 & 148
 - SEQ IDs 22 to 28 disclosed in reference 1 as SEQ IDs 88, 95, 101, 107, 96, 108 & 149
 - SEQ IDs 29 to 31 disclosed in reference 1 as SEQ IDs 89, 90 & 109
 - SEQ IDs 32 to 37 disclosed in reference 1 as SEQ IDs 10, 11, 12, 7, 8 & 9
- 10 SEQ IDs 38 to 50 disclosed in reference 1 as SEQ IDs 28-37, 39, 41 & 43
 - SEQ ID 75 disclosed in reference 3 as SEQ ID 1.

ABSTRACT

A nucleic acid vector comprising: (i) a promoter; (ii) a sequence encoding a HML-2 polypeptide operably linked to said promoter; and (iii) a selectable marker. Preferred vectors comprise: (i) a eukaryotic promoter; (ii) a sequence encoding a HML-2 polypeptide downstream of and operably linked to said promoter; (iii) a prokaryotic selectable marker; (iv) a prokaryotic origin of replication; and (v) a eukaryotic transcription terminator downstream of and operably linked to said sequence encoding a HML-2 polypeptide. Vectors of the invention are particularly useful for expression of HML-2 polypeptides either in vitro (e.g. for later purification).or in vivo (e.g. for nucleic acid immunization). They are well suited to nucleic acid immunization against prostate tumors. A preferred HML-2 is PCAV, which is located in chromosome 22 at 20.428 megabases (22q11.2).

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- 101. EP-A-0735898
- 102. EP-A-0761231
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FIGURE 1

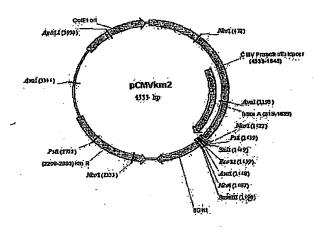


FIGURE 2

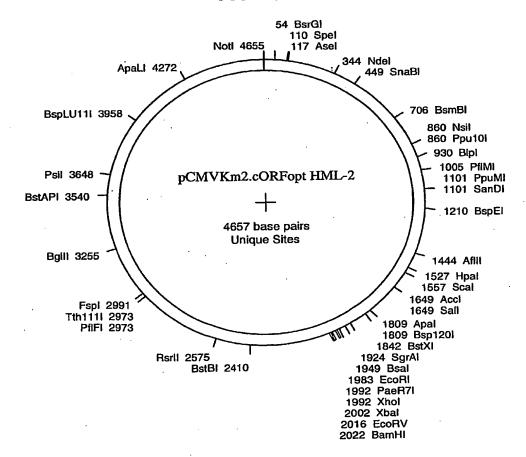


FIGURE 3

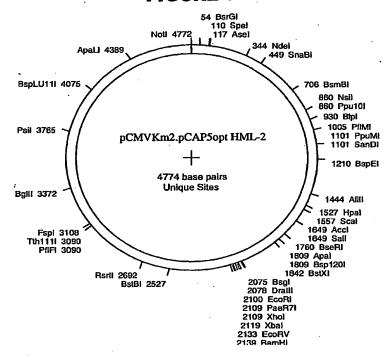
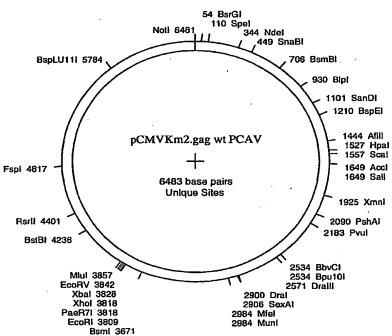


FIGURE 4



3/7

FIGURE 5

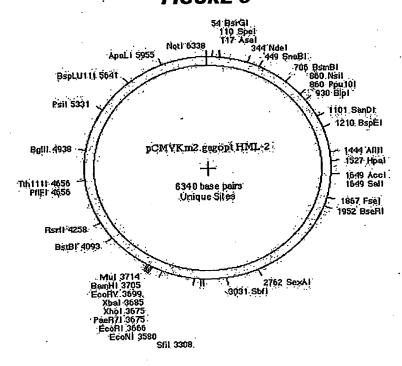


FIGURE 6

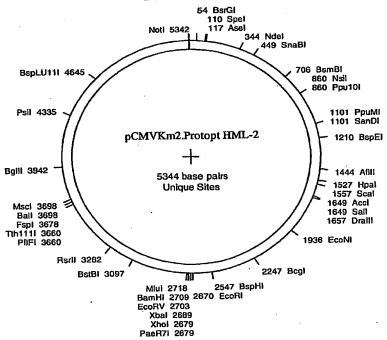


FIGURE 7

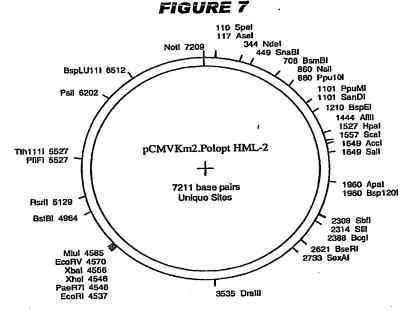


FIGURE 8

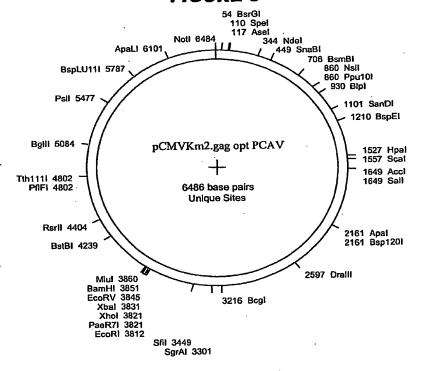


FIGURE 9

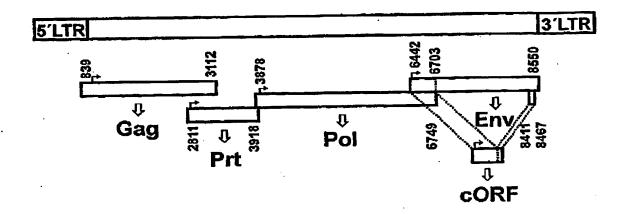


FIGURE 10

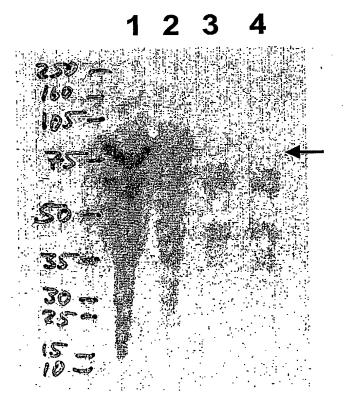


FIGURE 11A

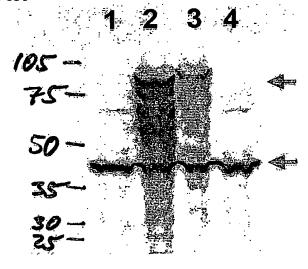
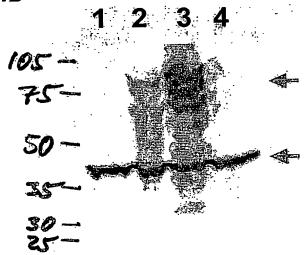


FIGURE 11B





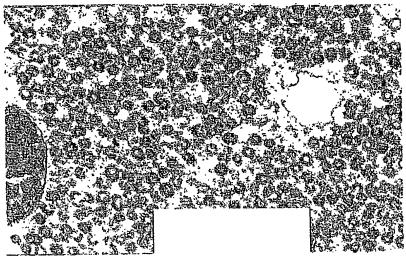
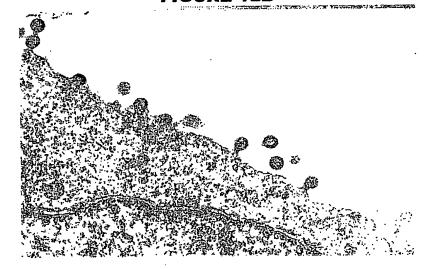


FIGURE 12B



SEQUENCE LISTING

SEQ ID 1

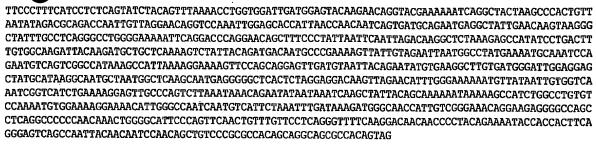
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SEQ ID 2

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SEQ ID 3

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SEQ ID 4

SEQ ID 5

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SEQ ID 6

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SEQ ID 7

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SEO ID 9

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SEQ ID 11

SEQ ID 12

SEQ ID 13

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SEQ ID 14

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SEQ ID 15

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SEQ ID 16

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SEQ ID 18

ATGGGGCCTCTCCAACCCGGGTTGCCCTCTCCGGCCATGATCCCAAAAGATTGGCCTTTAATTATAATTGATCTAAAGGATTGCTTTTTTACCATCC GGGAATGCTTAATAGTCCAACTATTTGTCAGACTTTTGTAGGTCGAGCTCTTCAACCAGTGAGAAAAGTTTTCAGACTGTTATATTCATTAT CATCCGATAAGATCCAAACCTCTACTCCTTTTCATTATTTAGGGATGCAGATAGAAAAATGAAAAATTAAGCCACAAAAAAATAAGAAAAAAGA CACATTAAAACACTAAATGATTTCAAAAATTACTAGGAGATATTAATTGGATTCGGCCAACTCTAGGCATTCCTACTTATGCCATGTCAAATTTG TTCTCTATCTTAAGAGGAGACTCAGACTTAAATAGTCAAAGAATATTAACCCCAGAGGCAACAAAAGAAATTAAATTAGTGGAAGAAAAAATTCAGT CAGCGCAAATAAATAGAATACATCCCTTAGCCCCACTCCAACTTTTGATTTTTGCCACTGCACATTCTCCAACAGGCATCATTATTCAAAATACTGA TCTTGTGGAGTGGTCATTCCTTCCTCACAGTACAGTTAAGACTTTTACATTGTACTTGGATCAAATAGCTACATTAATCGGTCAGACAAGATTACGA ATAACAAAATTATGTGGAAATGACCCAGACAAAATAGTTGTCCCTTTAACCAAGGAACAAGTTAGACCATTTATCAATTCTGGTGCATGGCAGA ${\tt TTGGTCTTGCTAATTTTGTGGGACTTATTGATAATCATTACCCAAAAACAAAGATCTTCCAGTTCTTAAAATTGACTACTTGGATTCTACCTAAAAT$ CATATGTACAGGCTACAAGGGATGTTGAGACAGCTCTAATTAAATATAGCATGGATGATCAGTTAAACCAGCTATTCAATTTACTACAACAAC TGTAAGAAAAAGAAATTTCCCATTTTATATTACTTATATTCGAGCACACACTAATTTACCAGGGCCTTTGACTAAAGCAAATGAACAAGCTGACTTA AGGCAAAAGATATTGTACAACATTGCACCCAGTGTCAAGTCTTACACCTGCCCACTCAAGAGGCAGGAGTTAATCCCAGAGGTCTGTGTCCTAATGC ATTATGGCAAATGGATGTCACGCATGTACCTTCATTTGGAAGATTATCATATGTTCATGTAACAGTTGATACTTATTCACATTTCATATGGGCAACT TGCCAAACAGGAGAAAGTACTTCCCATGTTAAAAAACATTTATTGTCTTGTTTTGCTGTAATGGGAGTTCCAGAAAAAATCAAAACTGACAATGGAC CAGGATATTGTAGTAAAGCTTTCCAAAAATTCTTAAGTCAGTGGAAAATTTCACATACAACAGGAATTCCTTATAATTCCCAAGGACAGGCCATAGT TGAAAGAACTAATAGAACACTCAAAACTCAATTAGTTAAACAAAAAGAAGGGGGGAGACAGTAAGGAGTGTACCACTCCTCAGATGCAACTTAATCTA GCACTCTATACTTTAAATTTTTTAAACATTTTATAGAAATCAGACTACTACTTCTGCAGAACAACATCTTACTGGTAAAAAGAACAGCCCACATGAAG GAAAACTAATTTGGTGGAAAGATAATAAAAATAAGACATGGGAAATAGGGAAGGTGATAACGTGGGGGGAGAGGTTTTGCTTGTGTTTCACCAGGAGA AAATCAGCTTCCTGTTTGGTTACCCACTAGACATTTGAAGTTCTACAATGAACCCATCGGAGATGCAAAGAAAAGGGCCTCCACGGAGATGCTAACA CCAGTCACATGGATGGATAATCCTATAGAAGTATATGTTAATGATAGTATATGGGTACCTGGCCCCATAGATGATCGCTGCCCTGCCCAAACCTGAGG AAGAAGGGATGATAAATATTTCCATTGGGTATCGTTATCCTCCTATTTGCCTAGGGAGGCACCAGGATGTTTAATGCCTGCAGTCCAAAATTG GTTGGTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCACGGGTAAATTATTACAAGAC TTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAATTCCCAAAGAATCAAAAAAATACAGAAGTTTTAGTTTGGG AAGAATGTGTGGCCAATAGTGCGGTGATATTATAAAACAATGAATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACAATTGCTC AGGACAAACTCAGTCGTGTCCAAGTGCACAAGTGAGTCCAGCTGTTGATAGCGACTTAACAGAAAGTTTAGACAAACATAAGCATAAAAAAATTGCAG TCTTTCTACCCTTGGGAATGGGGAAAAAGGAATCTCTACCCCAAGACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGA GGCTTACTGTGGCCTCACCACCACTTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATTGTAAGCCATTTTATACTGTCGACCTAAATTC ${\tt CAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATATGCTAGTTGTAGGAAATATAGTTATTAAACCAGACTCCCAGACTATAACCTGT$ GAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGTATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGT CCATGGACCGACGTGGGAGGCCTCACCATCCGTCCATATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTT GATTGGCAAAAGAATTCTACAAGATTGTGGAATTCACAATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTTAGACAAACTGTCATTT ${\tt GGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTCAGATTTTTGTATTACACCCCAAATTTATAATGA}$ GTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAGAAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAACAAATTTTCGAA GCATCAAAAGCCCATTTAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAGA CCATTGGAAGTACATCGATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTTAGTCTGCAGGTGTACCCAACAGCTCCGAAGAGAGA CAGCGACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCGAAAAGAAAAGGGGGGAAATGTGGGGAAAAGCAAGAGAAATTGTTACT **GTGTCTGTGTAG**

SEQ ID 19

MLTDLRAVNAVIQPMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQ PVREKFSDCYIIHGIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDTLKTLNDFQKLLGDINWI RPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEEKIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLY

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LDQIATLIGQTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIFQFLKLTTWILPKITRREPLENALTVFTDGSS
NGKAAYTGPKERVIKTPYQSAQRAELVAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYITHIRAHTN
LPGPLTKANEQADLLVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIVQHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYV
HVTVDTYSHFIWATCQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQGQAIVERTNRTLKTQLVKQKEGG
DSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLTGKKNSPHEGKLIWWKDSKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEP
IRDAKKSTSAETETSQSSTVDSQDEQNGDVRRTDEVAIHQEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCS

SEQ ID 20

MGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHY IDDILCAAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDTLKTLNDFQKLLGDINWIRPTLGIPTYAMSNL FSILRGDSDLNSQRILTPEATKEIKLVEEKIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIATLIGQTRLR ITKLCGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFVGLIDNHYPKTKIFQFLKLTTWILPKITREPLENALTVFTDGSSNGKAAYTGPKERVI KTPYQSAQRDELVAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYITYIRAHTNLPGPLTKANEQADL LVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIVQHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWAT CQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQGQAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNL ALYTLNFLNIYRNQTTTSAEQHLTGKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWLPTRHLKFYNEPIGDAKKRASTEMVT PVTWMDNPIEVYVNDSIWVPGPIDDRCPAKPEEEGMMINISIGYRYPPICLGRAPGCLMPAVQNWLVEVPTVSPISRFTYHMVSGMSLRPRVNYLQD FSYQRSLKFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILXNNEFGTIIDWAPRGQFYHNCSGQTQSCPSAQVSPAVDSDLTESLDKHKHKKLQ SFYPWEWGEKGISTPRPKIVSPVSGPEHPELWRLTVASHHIRIWSGNQTLETRDCKPFYTVDLNSSLTVPLQSCVKPPYMLVVGNIVIKPDSQTITC ENCRLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKGVLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVN DWQKNSTRLWNSQSSIDQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRHLQGREDNLTLDISKLKEQIFE ASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTSIINLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVT VSV

SEQ ID 21

NKSRKRRNRESLLGAATVEPPKPIPLTWKTEKPVWVNQWPLPKQKLEALHLLANEQLEKGHIEPSFSPWNSPVFVIQKKSGKWRMLTDLRAVNAV1Q
PMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIH
CIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDTLKTLNDFQKLLGDINWIRPTLGIPTYAMSN
LFSILRGDSDLNSKRMLTPEATKEIKLVEEKIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIATLIGQTRL
RIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIFQFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERV
IKTPYQSAQRAELVAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYITHIRAHTNLPGPLTKANEQAD
LLVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIVQHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWA
TCQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQGQAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLN
LALYTLNFLNIYRNQTTTSAEQHLTGKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPIRDAKKSTSAETE
TSQSSTVDSQDEQNGDVRRTDEVAIHQEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCS

SEQ ID 22

ATGAACCCATCAGAGATGCAAAGAAAAAGCACCTCCGCGGAGACGGCGACCATCGCAATCGACCGCTTGACTCACAAGATGAACAAAATGGTGACGT CAGAAGAACAGATGAAGTTGCCATCCACCAAGAAGGCCAGAGCCGCCAACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAAATATCTAGA GAACACAAAGGTGACACAAACCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCT GCAGCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGATAATCCTACAGAAGTATATGTTAATGATA CACATGGTAAGCGGGATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTT GCCCCAAGGAAATTCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATGAATT CGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAGTGTGCCAAGTGCACAAGTGAGTCCAGCTGTT GATAGCGACTTAACAGAAAGTTTAGACAAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAGGAATCTCTACCCCAA GACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCCTCACACCACCATTAGAATTTGGTCTGGAAATCA AACTTTAGAAACAAGAGATCGTAAGCCATTTTATACTATTGACCTGAATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATATG CTAGTTGTAGGAAATATAGTTATTAAACCAGACTCCCAGACTATAACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGC TGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATTGCGGTTAATTGCAGTCACAGCTACGGCTGCT GTAGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGATTGGCAAAAAAATTCTACAAGATTGTGGAATTCACAATCTAGTA ATGTGACTGGAATACGTCAGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGA GAAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAACAAATTTTCGAAGCATCAAAAGCCCATTTAAATTTTGGTGCCAGGAACTGAGGCAATTG CAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAGACCATTGGAAGTACTACGATTATAAATCTCATATTAATCCTTGTGTG CCTGTTTTGTCTGTTGTTAGTCTGCAGGTGTACCCAACAGCTCCGAAGAGACAGCGACCA





ATGCAAAGAAAAGCACCTCCGCGGAGACACGGAGACATCGCAATCGAGCACCGTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAACAGATGA AGTTGCCATCCACCAAGAAGGCAGAGCCGCCAACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAAATATCTAGAGAACACAAAGGTGAC ACAAACCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCAGCTAACTATACC GCCCCATAGATGATCGCTGCCCTGCCCAAACCTGAGGAAGAAGGGATGATGATAAATATTTCCATTGGGTATCATTATCCTCCTATTTGCCTAGGGAG ATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAATTC CCAAAGAATCAAAAAATACAGAAGTTTTAGTTTTGGGAAGAATGTGTGGCCCAATAGTGCGGTTGATATTACAAAACAATGAATTCGGAACTATTATAGA TTGGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAGTCGTGTCAAAGTGCACAAGTGAGTCCAGCTGTTGATAGCGACTTAACA GAAAGTTTAGACAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCCTTGGGAATGGGGAGAAAAAGGAATCTCTACCCCAAGACCAAAAATAGTAA GTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCCTCACCACCACTTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAG AGATCGTAAGCCATTTTATACTATTGACCTGAATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATATGCTAGTTGTAGGAAAT ATAGTTATTAAACCAGACTCCCAGACTATAACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGTATTCTGC TGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGATTAATTGCAGTCACAGCTACGGCTGCTGTAGCAGGAGTTGCA TTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGATTGGCAAAAAAATTCTACAAGATTGTGGAATTCACAATCTAGTATTGATCAAAAATTGG GTCAGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAGAAGATAATCTCACT TTAGACATTTCCAAATTAAAAGAACAAATTTTCGAAGCATCAAAAGCCCATTTAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATG GCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAGACCATTGGAAGTACTACGATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTT GTTAGTCTGCAGGTGTACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGCGGTTTTGTCGAAAAGAAAAGGGGGA

SEQ ID 24

GTCACATGGATGATGATATCCTATAGAAGTATATGTTAATGATAGTGTATGGGTACCTGGCCCACAGATGATCGCTGCCCTGCCCAAACCTGAGGAAG AAGGGATGATAAATATTTCCATTGTGTATCGTTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAATGCCTGCAGTCCAAAATTGGTT GGTAGAAGTACCTACTGTCAGTCCTAACAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTT TCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAATTCCCAAAGAATCAAAAAAATACAGAAGTTTTAGTTTGGGAAG AATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATGAATTCGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGG ACAAACTCAGTCGTGTCCAAGTGCACAAGTGAGTCCAGCTGTTGATAGCGACTTAACAGAAAGTCTAGACAAACATAAGCATAAAAAATTACAGTCT TTCTACCCTTGGGAATGGGGAGAAAAAGGAATCTCTACCCCAAGACCAGAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGC ${\tt TTTGGCCTGACACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATCGTAAGCCATTTTATACTATCGACCTAAATTCCAGTCTA}\ .$ ACGGTTCCTTTACAAAGTTGCGTAAAGCCCTCTTATATGCTAGTTGTAGGAAATATAGTTATTAAACCAGACTCCCAAACTATAACCTGTGAAAAATT CTGACCGTGGGAGGCCTCGCCATCCATCCATATTTTGACTGAAGTATTAAAAGACATTTTAAATAGATCCAAAAGATTCATTTTTACCTTAATTGCA GTGATTATGGGATTAATTGCAGTCACAGCTACGGCTGCTGTGGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCGGTAAACTTTGTTAATGATTGGC AAAAGAATTCTACAAGATTGTGGAATTCACAATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTTAGACAAACTGTCATTTGGATGGG AGACAGACTCATGAGCTTAGAACATTGTTTCCAGTTACAGTGTGACTGGAATACGTCAGATTTTTGTATTACACCCCAAATTTTATAATGAGTCTGAG CATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAGAGATAATCTCACTTTAGACATTTCCAAATTAAAATAACAAATTTTCGAAGCATCAA AAGCCCATTTAAATTTGATGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTTAACCCTGTCACTTGGGTTAAGACCATCGG AAGTACTATGATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTTGTTGCTGCAGGTGTACCCAACAGCTCCGAAGAGACAGCACCAC CATCGAGAACGGGCCA

SEQ ID 25

TGTAAGAAAAGAAATTTCCCATTTTATATTACTTATATTCGAGCACACACTAATTTACCAGGGCCTTTGACTAAAGCAAATGAACAAGCTGACTTA $\tt CTGGTATCATCTGCACTCATAAAAGCACAAGAACTTCATGCTTTGACTCATGTAAATGCAGCAGGATTAAAAAAACAAATTTGATGTCACATGGAAAC$. AGGCAAAAGATATTGTACAACATTGCACCCAGTGTCAAGTCTTACACCTGCCCACTCAAGAGGCAGGAGTTAATCCCAGAGGTCTGTGTCCTAATGCATTATGGCAAATGGATGTCACGCATGTACCTTCATTTGGAAGATTATCATATGTTCATGTAACAGTTGATACTTATTCACATTTCATATGGGCAACT TGCCAAACAGGAGAAAGTACTTCCCATGTTAAAAAACATTTATTGTCTTGTTTTTGCTGTAATGGGAGTTCCAGAAAAAATCAAAACTGACAATGGAC ${\tt CAGGATATTGTAGTAAAGCTTTCCAAAAATTCTTAAGTCAGTGGAAAATTTCACATACAACAGGAATTCCTTATAATTCCCAAGGACAGGCCATAGT$ TGAAAGAACTAATAGAACACTCAAAACTCAATTAGTTAAACAAAAAGAAGGGGGGAGACAGTAAGGAGTGTACCACTCCTCAGATGCAACTTAATCTA GCACTCTATACTTTAAATTTTTTAAACATTTATAGAAATCAGACTACTACTTCTGCAGAACAACATCTTACTGGTAAAAAGAACAGCCCACATGAAG GAAAACTAATTTGGTGGAAAGATAATAAAAATAAGACATGGGAAATAGGGAAGGTGATAACGTGGGGGAGAGGTTTTGCTTGTGTTTCACCAGGAGA AAATCAGCTTCCTGTTTGGTTACCCACTAGACATTTGAAGTTCTACAATGAACCCATCGGAGATGCAAAGAAAAGGGCCTCCACGGAGATGGTAACA CCAGTCACATGGATGATAATCCTATAGAAGTATATGTTAATGATAGTATATGGGTACCTGGCCCATAGATGATCGCTGCCCTGCCAAACCTGAGG AAGAAGGGATGATAAATATTTTCCATTGGGTATCGTTATCCTCCTATTGCCTAGGGAGAGCACCAGGATGTTTAATGCCTGCAGTCCAAAATTG GTTGGTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCCACGGGTAAATTATTTACAAGAC TTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAATTCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGG AAGAATGTGTGGCCAATAGTGCGGTGATATTATAAAACAATGAATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACAATTGCTC AGGACAAACTCAGTCGTGTCCAAGTGCACAACTGAGTCCAGCTGTTGATAGCGACTTAACAGAAAGTTTAGACAAACATAAGCATAAAAAAATTGCAG TCTTTCTACCCTTGGGAATGGGGAGAAAAGGAATCTCTACCCCAAGACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGA GGCTTACTGTGGCCTCACACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATTGTAAGCCATTTTATACTGTCGACCTAAATTC CAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATATGCTAGTTGTAGGAAATATAGTTATTAAACCAGACTCCCAGACTATAACCTGT GAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGTATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGT CCATGGACCGACGTGGGAGGCCTCACCATCCGTCCATATTTTGACTGAAGTATTAAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTT GATTGGCAAAAGATTCTACAAGATTGTGGAATTCACAATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTTAGACAAACTGTCATTT GGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTCAGATTTTTGTATTACACCCCCAAATTTATAATGA GTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAGAAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAACAAATTTCGAA GCATCAAAAGCCCATTTAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAGA GTGTCTGTGTAG

SEQ ID 26

MQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAANYT
YWAYVPFPPLIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGYHYPPICLGRAPGCLMPAVQNWLVEVPTVSPICRFTYHMVSG
MSLRPRVNYLQDFSYQRSLKFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQSCQSAQVSPAVDSDLT
ESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPELWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYMLVVGN
IVIKPDSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKGVLNRSKRFIFTLIAVIMGLIAVTATAAVAGVA
LHSSVQSVNFVNDWQKNSTRLWNSQSSIDQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRHLQGREDNLT
LDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTIINLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGG
NVGKSKRDQIVTVSV

SEQ ID 27

MGPLQPGLPSPAMIPKDWPLITIDLKDCFFTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHY
IDDILCAAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDTLKTLNDFQKLLGDINWIRPTLGIPTYAMSNL
FSILRGDSDLNSQRILTPEATKEIKLVEEKIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIATLIGQTRLR
ITKLCGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFVGLIDNHYPKTKIFQFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVI
KTPYQSAQRDELVAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYITYIRAHTNLPGPLTKANEQADL
LVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIVQHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWAT
CQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQGQAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNL
ALYTLNFLNIYRNQTTTSAEQHLTGKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWLPTRHLKFYNEPIGDAKKRASTEMVT
PVTWMDNPIEVYVNDSIWVPGPIDDRCPAKPEEEGMMINISIGYRYPPICLGRAPGCLMPAVQNWLVEVPTVSPISRFTYHMVSGMSLRPRVNYLQD
FSYQRSLKFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILXNNEFGTIIDWAPRGQFYHNCSGQTQSCPSAQVSPAVDSDLTESLDKHKHKKLQ
SFYPWEWGEKGISTPRPKIVSPVSGPEHPELWRLTVASHHIRIWSGNQTLETRDCKPFYTVDLNSSLTVPLQSCVKPPYMLVVGNIVIKPDSQTITC
ENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKGVLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVN
DWQKNSTRLWNSQSSIDQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRHLQGREDNLTLDISKLKEQIFE
ASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTSIINLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVT
VSV

SEQ ID 28

MNPSEMORKAPPRRRHRNRAPLTHKMNKMVTSEEOMKLPSTKKAEPPTWAOLKKLTOLATKYLENTKVTOTPESMLLAALMIVSMVVSLPMPAGAA AANYTYWAYVPFPPLIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGYHYPPICLGRAPGCLMPAVONWLVEVPTVSPICRFTY

HMVSGMSLRPRVNYLQDFSYQRSLKFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQSCPSAQVSPAV
DSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPELWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYM
LVVGNIVIKPDSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKGVLNRSKRFIFTLIAVIMGLIAVTATAA
VAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSIDQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRHLQGR
EDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTIINLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLS
KRKGGNVGKSKRDQIVTVSV

SEQ ID 29

AGTTCTACAATGAACCCATCAGAGATGCAAAGAAAAGCACCTCCGCGGAGACGGAGACATCGCAATCGAGCACCGTTGACTCACAAGATGAACAAAA TGGTGACGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAGGCAGGAGCCGCCAACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAA ATATCTAGAGAACACAAAGGTGACACAAACCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCA GGA

SEQ ID 30

TCTGCAGGTGTACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGCCATGA

SEQ ID 31

MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAGPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVSAGVPNSSEE TATIENGP

SEQ ID 32

 ${\tt MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKSAGVPNSSEETATIENGP}$

SEQ ID 33

MNPSEMORKGPPORCLOVYPTAPKRORPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVLY

SEQ ID 34

MNSLEMORKVWRWRHPNRLASLQVYPAAPKRQQPARMGHSDDGGFVKKKRGGYVRKREIRLSLCLCRKGRHKKLHFVLY

SEQ ID 35

 ${\tt MNPSEMQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVILQVYPTAPKRQRPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVLY$

SEQ ID 36

 ${\tt MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVYPTAPKRQRPSRTGHDDDGGFVEKKRGK\\ {\tt CGEKQERSDCYCVCVERSRHRRLHFVLY}$

SEQ ID 37

MNPSEMORKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVYPTAPKRQR PSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVLY

SEQ ID 38

MNPSEMQRKGPPQRCLQVYPTAPKRQRPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVLY

SEQ ID 39

MNPSEMQRKGPPQRCLQVYPTAPKRQRPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVLY

SEQ ID 40

MEYKNRHLKFYNEPIGDAKKRASTEMSAGVPNSSEETATIENGP

SEQ ID 41

 ${\tt MNPSEMQRKGPPQRCLQVYPTAPKRQRPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVLY}$

SEQ ID 42

 ${\tt MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKSAGVPNSSEETATIENGP}$

SEQ ID 43

MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVSAGVPNSSEE
TATIENGP

SEQ ID 44

MVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYPPICLGRAPGCLMPAVQNCLQVYPTAPKRQRPSRTGHDDDGGFVEKKR GKCGEKQERSDCYCVCVERSRHRRLHFVLY

SEQ ID 45

 ${\tt MVTPVTWMDNPIEVYVNDSEWVPGPTDDRCPAKPEEEGMMINISIGLQVYPTAPKRQRPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRLHFVMC$

SEQ ID 46

 ${\tt MNSLEMQRKVWRWRHPNRLASLQVYPAAPKRQQPARMGHSDDGGFVKKKRGGYVRKREIRLSLCLCRKGRHKKLHFDLY}$

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SEQ ID 47

MNSLEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLSSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAA AANYTYWAYVPFPPLIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGYHYPPICLGRAPGCLMPAVQNWLVEVPTVSPICRFTY HMSAGVPNSSEETATIENGP

SEQ ID 48

 ${\tt MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVTLQVYPTAPKRQRPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVMY$

SEQ ID 49

 $\verb|mnpsemQrkapprrrrhrnraplthkmnkmvtseeqmklpstkkaepptwaqlkkltqlatkylentkvyptapkrqrpsrtghdddggfvekkrgk cgekoersdcycvcversrhrrlhfvmy$

SEQ ID 50

MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYXLENTKVTQTPESMLLAALMIVSMVVYPTAPKRQ RPSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVMY

SEQ ID 51

GCCGCGGAATTTCGACTCTAGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCATGTTGA CATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG GCCCGCCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCA ATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGG ${\tt CCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT}$ AAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAAC GTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGTGATGGTATAGCCTATAGCCTATAGGTGTGGTTATTGACCAC TCCCCTATTGGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTGGCTATATGCCAATACTCTGTCCTTCAG AGACTGACACGGACTCTGTATTTTTACAGGATGGGGTCCCATTTATTATTACAAATTCACATATACAACACGCCGTCCCCCGTGCCCGCAGTTTT TATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGGGCTCTTCTCCGGTAGCGGCGAGCTTCCACATCCGAGCCCT GGTCCCATGCCTCCAGCGGCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAACAATGCCCACCACCACCAG GCAGAAGAAGATGCAGCCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCT ${\tt GAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAGTCACCGTCG}$ qatqqtqaccaqcqaqqaqcagatqaagctgcccagcaccaagaaggccgagccccccacctgggcccagctgaagaagctgacccagctggccacc aagtacctqqaqaacaccaaqqtqacccaqaccccqaqaqcatqctqctqccqccctqatqatcqtqagcatqgtqagcqccqgcgtgcccaaca qcaqcqaqqaqaccqccatcqaqaacqqccccqcttaaaqaattcAGACTCGAGCAAGTCTAGAAAGCCATGGATATCGGATCCACTACGCGTT ${\tt CCACTGTCCTTTCCTAATAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGCAGGACAGCAAGGGCAAGGGCAAGGGAAGTGCATTGCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGAAGTGCATTGCTATTCTGGGGGGGTGGGGTGGGGAAGTGCAAGGGAAATTGCATCGCATTGTCTGAGTAGGTTGCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGAAGTGCAATTGC$ GGAGGATTGGGAAGACAATAGCAGGGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAAACGAT $\tt CCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTC$ GCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGACAGTCGATGAATCCAGAAAAAG CGGCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACA ${\tt GTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGATGCGATGCTTTT}$ CGCTTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCTTTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGA GATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG TGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCG TGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAG ${\tt CTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTTGCGCTTGCGTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGT$ CAGCACCGTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTGAAGCTAATTCATGGT TAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGCCCGAGATAGGGTTGAGTGT GCTGCGGCGAGCGGTATCAGCTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAG CAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAAATCGACGCTCAAGTCAGA GGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATA

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SEQ ID 52

GCCGCGGAATTTCGACTCTAGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCATGTTGA ${\tt CATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG}$ ${\tt GCCCGCCTGGCTGACCGCCCAACGACCGCCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAGTTCCCATAGTAACGCCCAATAGGGACTTTCCATTGACGTCAATAGTTCAATAGTAACGCCCAATAGGGACTTTCCATTGACGTCAATAGTTCAATAGATGACGTCAATAGTTCAATAGTAATGACGTCAATAGTTCAATAGTAATGACGTCAATAGTTCAATAGTAATGACGTCAATAGTTCAATAGTAATGACGTCAATAGTTCAATAGTTCAATAGTTCAATAGTAATGACGTCAATAGTTCAATA$ ATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCTATTGACGTCAATGACGGTAAATGG $\tt CCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT$ AAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCAGGAAC TCCCCTATTGGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTGGCTATATGCCAATACTCTGTCCTTCAG AGACTGACACGGACTCTGTATTTTTACAGGATGGGGTCCCATTTATTATTTACAAATTCACATATACAACGCCGTCCCCCGTGCCCGCAGTTTT ${\tt TATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGGGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCT\\$ TGTGCCGCACAGGCCGTGGCGGTAGGGTATGTGTCTGAAAATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCG ${\tt GCAGAAGAAGATGCAGCCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCT}$ GAGCAGTACTCGTTGCTGCCGCGCGCCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAGTCACCGTCG $\verb|tcgacgccaccatgaaccccagcgagatgcagcgccaccgccgccgccgccgccgccaccgcaaccgcgccccctgacccacaagatgaacaa|$ gatggtgaccagcgaggagcagatgaagctgcccagcaccaagaaggccgagcccccccacctgggcccagctgaagaagctgacccagctggccacc aagtacctggagaacaccaaggtgacccagacccccgagagcatgctggtggccgccctgatgatcgtgagcatggtggtgtaccccaccqccccca agcgccagcgcccagccgccaccggccacgacgacgacggcgttcgtggagaagaagcgcggcaagtgcggcgagaagcaggagcgcagcgactg $\verb|ctactgcgtgtgcgtggagcgcagccgccaccgccgcctgcacttcgtgctgtacgcttaaagaattcAGACTCGAGCAAGTCTAGAAAGCCATGGA|$ GTGGGGCAGGACAGCAAGGGGGGGTTGGGAAGACAATAGCAGGGGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAG CCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGCAAATCTCGTGATGGCAGGTTGGGCGTTGGTCGG TCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACG AGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCAC AGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCG $\tt CGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGT$ GCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCAC AGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCC ${\tt AAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCA}\\$ GATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTC CATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCAGATAGCCCAGT AGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCA GCGTGAAGCTAATTCATGGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAG CCCGAGATAGGGTTGAGTGTTGCTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGG GCGATGGCCGGATCAGCTTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGAC ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAA AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG ACCCTGCCGCTTACCGGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGG TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG CCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACTGAACG GTGATCCCCACCGGAATTGCG

EGDSZO. COLSTIDO





SEQ ID 53

GCCGCGGAATTTCGACTCTAGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCATGTTGA CATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG ATGGCTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGG ${\tt CCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT}$ AAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCACCGGAAC GTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGTGATGGTATAGCCTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCAC TCCCCTATTGGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTGGCTATATGCCAATACTCTGTCCTTCAG AGACTGACACGGACTCTGTATTTTTACAGGATGGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCAGTTTT TATTANACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGGGCTCTTCTCCGGTAGCGGGGGGGAGCTTCCACATCCGAGCCCT GGTCCCATGCCTCCAGCGGCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCACAATGCCCACCACCACCAG TGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAAATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCG qaqaaqatattqtttcaqtttctqatqcccctaaaaqctqtqtaacaqattqtqaaqaaqaqqcaqqqacaqaatcccaqcaaqqaacqqaaaqttc acattqtaaatatqtaqcaqaqtctqtaatqqctcaqtcaacqcaaaatqttqactacaqtcaattacaqgaqataatataccctqaatcatcaaaa ttgggggaaggaggtccagaatcattggggccatcagagcctaaaccacgatcgccatcaactcctcctcccgtggttcagatgcctgtaacattacaacctcaaacgcaggttagacaagcacaaaccccaagagaaaatcaagtagaaagggacagagtctctatcccggcaatgccaactcagatacagta tccacaatatcagccggtagaaaataagacccaaccgctggtagtttatcaataccggctgccaaccgagcttcagtatcggcctccttcagaggttcaatacagacctcaagcggtgtgtcctgtgccaaatagcacggcaccataccagcaacccacagcgatggcgtctaattcaccaqcaacacaggacg cggcgctgtatcctcagccgcccactgtgagacttaatcctacagcatcacgtagtggacagggtggtgcactqcatgcagtcattgatgaagccagattccattgctcatggaaatagacttactccttatgactgggaaattttggccaaatcttccctttcatcctctcagtatctacagtttaaaacctggtggattgatggagtacaagaacaggtacgaaaaaatcaggctactaagcccactgttaatatagacgcagaccaattgttaggaacaggtccaaat tggagcaccattaaccaaccaatcagtgatgcagaatgaggctattgaacaagtaagggctattttgcctcagggcctggggaaaaattcaggacccag gaacagctttccctattaattcaattagacaaggctctaaagagccatatcctgactttgtggcaagattacaagatgctgctcaaaagtctattac agatgacaatgcccgaaaagttattgtagaattaatggcctatgaaaatgcaaatccagaatgtcagtcggccataaaagccattaaaaggaaaagtt ccagcaggagttgatgtaattacagaatatgtgaaggcttgtgatgggattggaggagctatgcataaggcaatgctaatggctcaagcaatgaggg ggctcactctaggaggacaagttagaacatttgggaaaaaatgttataaattgtggtcaaatcggtcatctgaaaaggagttgcccagtcttaaataa tgtttgttcctcagggttttcaaggacaacaacccctacagaaaataccaccacttcagggagtcagccaattacaacaatccaacagctgtcccgc gccacagcagcagcaccgcagtaagaattcagactcgagcaagtctagaAAGCCATGGATATCGGATCCACTACGCGTTAGAGCTCGCTGATCAGC TAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACA ATAGCAGGGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTT TCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAG CAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCAT GATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCAGC ${\tt GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTG}$ AATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG CAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAAGCC CACTGCAAGCTACCTGCTTTCTCTTTTGCGCTTTCCCTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGG AGCTCATTTTTTAACCAATAGGCCGAAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGCCCGAGATAGGGTTGAGTGTTCCAGTTTGGAACA

SEQ ID 54

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GCCGCGGAATTTCGACTCTAGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTATATTGGCTCATGTCCAATATGACCGCCATGTTGA CATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG ${\tt GCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCATTGACGTCAATAATGACGTCAATAGTCAACGCCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAATGACGTCAATAGTCAACGCCCAATAGGGACTTTCCATTGACGTCAATAATGACGTCAATAATGACGTCAATAGTCAACGCCCAATAGGGGACTTTCCATTGACGTCAATAATGACGTCAATAATGACGTCAATAATGACGTCAATAGTCAACGCCCAATAGGGGACTTTCCATTGACGTCAATAATGACGTCAATAATGACGTCAATAGTCAACGCCCAATAGGGGACTTTCCATTGACGTCAATAATGACGTCAATAATGACGTCAATAGTCAACGCCCAATAGGGGACTTTCCAATTGACGTCAATAATGACGTCAATAGTCAATAGTCAATAATGACGTCAATAGTCAATAGTCAATAATGACGTCAATAGTCAATAGTCAATAATGACGTCAATAGTCAATAATGACGTCAATAGTCAATAATGACGTCAATAGTCAATAATGACGTCAATAGT$ GTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGTGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCAC TCCCCTATTGGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTGGCTATATGCCAATACTCTGTCCTTCAG A GACTGACACGGACTCTGTATTTTACAGGATGGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCAGTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGGGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCT ${\tt GCAGAAGAAGATGCAGCCAGCTGAGTTGTTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCT}$ ${\tt GAGCAGTACTCGTTGCTGCCGCGCGCGCCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAGTCACCGTCG}$ tcgacgccaccatgtgggccaccatcgtgggcaagcgcccaagggccccgccagcggcccaccaccaactggggcatccccaacagcgccatctgggcagegccgccgtggacctgtgcaccatccaggccgtgagcctgctgcccggcgagccccccagaagacccccaccggcgtgtacggcccctgc ccaagggcaccgtgggcctgatcctgggccgcagcagcctgaacctgaagggcgtgcagatccaccagcgtggtggacagcgactacaagggcga gatccagctggtgatcagcagcagcatcccctggagcgccagcccccgcgaccgcatcgcccagctgctgctgctgctgccctacatcaagggcggcaac aggccat categoggcaagcagttegagggcctggtggacaccggcgccgacgtgagcatcatcgccctgaaccagtggcccaagaactggcccaagcagaaggccgtgaccggcctggtgggcatcggcaccgccagcgaggtgtaccagagcaccgagatcctgcactgcctgggccccgacaaccaggag gctacagccccaccagccagaagatcatgaccaagatgggctacatccccggcaagggcctgggcaagaacgaggacggcatcaagatccccgtgga ggccaagatcaaccaggagcgcgagggcatcggcaacccctgcgcttaaagaattcAGACTCGAGCAAGTCTAGAAAGCCATGGATATCGGATCCAC GCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCCAGCCGGCCACAGTCGATGAATC CAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGG

AACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGG CAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCA TCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTGAAGCTAA TTCATGGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGCCCGAGATAGGG TTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAAACCGTCTATCAGGGCGATGGCCGGA TCAGCTTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTC AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT ACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC **GGAATTGCG**

SEQ ID 56

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SEQ ID 57

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GAACACCAAGGTGACCCAGACCCCCGAGAGCATGCTGCTGGCCGCCCTGATGATCGTGAGCATGGTGAGCGCCGGCGTGCCCAACAGCAGCAGCGAGGAG ACCGCCACCATCGAGAACGGCCCCGCTTAA

SEQ ID 59

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SEQ ID 60

GCGAGGAGCAGATGAAGCTGCCCAGCACCAAGAAGGCCGAGCCCCCACCTGGGCCCAGCTGAAGAAGCTGACCCAGCTGGCCACCAAGTACCTGGA GAACACCAAGGTGACCCAGACCCCCGAGAGCATGCTGCTGGCCGCCCTGATGATCGTGAGCATGGTGGTGTACCCCACCGCCCCCAAGCGCCAGCGC



 $\tt CCCAGCCGCACCGACGACGACGACGGCGCTTCGTGGAGAAGAAGCGCGGCAAGTGCGGCGAGAGCAGCGACGACTGCTACTGCGTGT$ GCGTGGAGCGCAGCCGCCACCGCCGCCTGCACTTCGTGCTGTACGCTTAA

SEQ ID 61

AAAATCTAATCAAGCTATTTCAAATAATAGAACAATTTTGCCCATGGTTTCCAGAACAAGGAACTTTAGATCTAAAAGATTGGAAAAGAATTGGTAA GGAACTAAAACAAGCAGGTAGGAAGGGTAATATCATTCCACTTACAGTATGGAATGATTGGGCCATTATTAAAGCAGCTTTAGAACCATTTCAAACA TACATTGCGAATATGTAGCAGAGCCGGTAATGGCTCAGTCAACGCAAAATGTTGACTATAATCAATTACAGGAGGTGATATATCCTGAAACGTTAAA $A \verb|TTAGAAGGAAAAGGTCCAGAATTAGTGGGGCCATCAGAGTCTAAACCACGAGGCACAAGTCCTCTTCCAGCAGGTCAGGTGCCTGTAACATTACAA$ AGTATGGATATCCAGGAATGCCCCCAGCACCACAGGGCAGGGCGCCCATACCCTCAGCCGCCCACTAGGAGACTTAATCCTACGGCACCACCTAGTAGAGTATGGACCCAACTCCCCTTATATGAGGACATTATTAGATTCCATTGCTCATGGACATAGACTCATTCCTTATGATTGGGAGATTCTGGCAAAATC ${\tt GTCTCTCTCACCCTCTCAATTTTACAATTTAAGACTTGGTGGATTGATGGGGTACAAGAACAGGTCCGAAGAAATAGGGCTGCCAATCCTCCAGTT$ AACATAGATGCAGATCAACTATTAGGAATAGGTCAAAATTGGAGTACTATTAGTCAACAAGCATTAATGCAAAAATGAGGCCATTGAGCAAGTTAGAG $\tt CTATCTGCCTTAGAGCCTGGGAAAAAATCCAAGACCCAGGAAGTACCTGCCCCTCATTAATACAGTAAGACAAGGTTCAAAAGAGCCCTATCCTGA$ ${\tt CCTGAGTGTCAATCAGCCATTAAGCCATTAAAAGGAAAGGTTCCTGCAGGATCAGATGTAATCTCAGAATATGTAAAAGCCTGTGATGGAATCGGAGATCGGAGATCAGATCAGAATATGTAAAAGCCTGTGATGGAATCGGAGATCAGATCAGAATCTCAGAATATGTAAAAGCCTGTGATGGAATCGGAGATCAGATCAGAATCTCAGAATATGTAAAAGCCTGTGATGGAATCGGAGATCAGAATCAGAATCTCAGAATATGTAAAAAGCCTGTGATGGAATCGGAGATCAGAATCAG$ TCAPATTGGTCACTTAPAAAAAAGAATTGCCCAGTCTTAPATAAACAGAATATAACTATTCAAGCAACTACAACAGGTAGAGAGCCACCTGACTTATGT $\tt CTCAGGCCCCACAACAACTGGGGCATTCCCAATTCAGCCATTTGTTCCTCAGGGTTTTCAGGGACAACCACCCCCACTGTCCCAAGTGTTTCAGGG$ AATAAGCCAGTTACCACAATACAACAATTGTCCCCCGCCACAAGCGGCAGTGCAGCAGTAG

SEQ ID 62

 $\tt ATGGGCCAGACCAAGAGCAAGATCAAGAGCAAGTACGCCAGCTACCTGAGCTTCATCAAGATCCTGCTGAAGCGCGGCGGCGTGAAGGTGAGCACCA$ A GAACCTGATCAAGCTGTTCCAGATCATCGAGCAGTTCTGCCCCTGGTTCCCCGAGCAGGGCACCCTGGACCTGAAGGACTGGAAGCGCATCGGCAATGCACTGCGAGTACGTGGCCGAGCCCGTGATGGCCCAGAGCACCCAGAACGTGGACTACAACCAGCTGCAGGAGGTGATCTACCCCGAGACCCTGAA GCTGGAGGGCCAGGGGCCCCGAGCTGGTGGCCCCAGCGAGAGCAAGCCCCGCGGCACCAGCCCCTGCCCGCCGGCCAGGTGCCCGTGACCCTGCAG CCATCTGCCTGCGCGCCTGGGAGAAGATCCAGGACCCCGGCAGCACCTGCCCCAGCTTCAACACCGTGCGCCAGGGCAGCAAGGAGCCCTACCCCGA $\tt CCAGATCGGCCACCTGAAGAAGAACTGCCCCGTGCTGAACAAGCAGAACATCACCATCCAGGCCACCACCACCACCGGCCGCGAGCCCCCGACCTGTGC$

SEQ ID 63

 ${\tt GTAGGACTAATCTTGGGACGATCAAGTCTAAATCTAAAAGGAGTTCAAATTCATACTAGTGTGGTTGATTCAGACTATAAAGGCGAAATTCAATTGG}$ TTATTAGCTCTTCAATTCCTTGGAGTGCCAGGAGACAGGATTGCTCAATTATTACTCCTGCCATACATTAAGGGTGGAAATAGTGAAATAAA AAGAATAGGAGGGCTTGGAAGCACTGATCCAACAGGAAAGGCTGCATATTGGGCAAGTCAGGTCTCAGAGAACAGACCTGTGTGTAAGGCCATTATT

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ACGAGTCAAAAAATCATGACCAAGATGGGATATATACCAGGAAAGGGGACTAGGGAAAAATGAAGATGGCATTAAAATTCCAGTTGAGGCTAAAATAAATCAAGAAAGAGAAGGAATAGGGAATCCTTGCTAG

SEQ ID 64

 ${\tt GTGGGCCTGATCCTGGGCCGCAGCAGCCTGAACCTGAAGGGCGTGCAGATCCACCAGCGTGGTGGACCAGCGACTACAAGGGCGAGATCCAGCTGG}$ TGATCAGCAGCAGCATCCCCTGGAGCGCCAGCCCCCGCGACCGCATCGCCCAGCTGCTGCTGCTGCCCTACATCAAGGGCGGCAACAGCGAGATCAA CAGGGCAAGCAGTTCGAGGGCCTGGTGGACACCGGCCGACGTGAGCATCATCGCCCTGAACCAGTGGCCCAAGAACTGGCCCAAGCAGAAGCAGAAGGCCG TGACCGGCCTGGTGGGCATCGGCACCGCCAGCGAGGTGTACCAGAGCACCGAGATCCTGCACTGCCTGGGCCCCGACAACCAGGAGAGCACCGTGCA ACCAGGAGCGCGAGGGCATCGGCAACCCCTGCGCTTAA

SEQ ID 65

ATGAATAAATCAAGAAAGGAAAGGAATAGGGAATCCTTGCTAGGGGCCGCCACTGTAGAGCCTCCTAAACCCATACCATTAACTTGGAAAACAGAAA AACCAGTGTGGGTAAATCAGTGGCCGCTACCAAAACAAAAACTGGAGGCTTTACATTTATTAGCAAATGAACAGTTAGAAAAAGGGTCATATTGAGCC ${\tt TTCGTTCTCACCTTGGAATTCTCCTGTGTTTGTAATTCAGAAGAAATCAGGCAAATGGCGTATGTTAACTGACTTAAGGGCTGTAAACGCCGTAATT$ ${\tt ACCTCAGGGAATGCTTAATAGTCCAACTATTTGTCAGACTTTTGTAGGTCGAGCTCTTCAACCAGTTAGAGAAAAGTTTTCAGACTGTTATATTATT$ CAATAGCATCTGATAAGATCCAAACCTCTACTCCTTTTCATTATTTAGGGATGCAGATAGAAAATAGAAAAATTAAGCCACAAAAAAATAGAAATAAG AAAAGACACATTAAAAACACTAAATGATTTTCAAAAATTACTAGGAGATATTAATTGGATTCGGCCAACTCTAGGCATTCCTACTTATGCCATGTCA AATTTGTTCTCTATCTTAAGAGGAGACTCAGACTTAAATAGTAAAAGAATGTTAACCCCAGAGGCAACAAAAGAAATTAAATTAGTGGAAGAAAAAA TTCAGTCAGCGCAAATAAATAGAATAGAATAGCCCCTTAGCCCCACTCCAACTTTTGATTTTTGCCACTGCACATTCTCCAACAGGCATCATTATTCAAAA TACTGATCTTGTGGAGTGGTCATTCCTTCCTCACAGTACAGTTAAGACTTTTACATTGTACTTGGATCAAATAGCTACATTAATCGGTCAGACAAGA TTACGAATAATAAAATTATGTGGGAATGACCCAGACAAAATAGTTGTCCCTTTAACCAAGGAACAAGTTAGACAAGCCTTTATCAATTCTGGTGCAT TAAAATTACCAGACGTGAACCTTTAGAAAATGCTCTAACAGTATTTACTGATGGTTCCAGCAATGGAAAAGCAGCTTACACAGGACCGAAAGAACGA $\textbf{ATTCTGCATATGTAGTACAGGCTACAAGGGATGTTGAGACAGCTCTAATTAAATATAGCATGGATGATCAGTTAAACCAGCTATTCAATTTATTACA$ TAATGCATTATGGCAAATGGATGTCACGCATGTACCTTCATTTGGAAGATTATCATATGTTCACGTAACAGTTGATACCTTATTCACATTTCATATGG $\textbf{ATGGACCAGGATATTGTAGTAAAGCTTTCCAAAAATTCTTAAGTCAGTGGAAAATTTCACATACAACAGGAATTCCTTATAATTCCCAAGGACAGGC$ AATCTAGCACTCTATACTTTAAATTTTTTAAACATTTATAGAAATCAGACTACTACTTCTGCAGAACAACATCTTACTGGTAAAAAAGAACAGCCCAC GAGACATCGCAATCGAGCACCGTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAGACGCCG CCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCAGCTAA

 $\tt CCATCGCCAGCGACAAGATCCAGACCAGCACCCCCTTCCACTACCTGGGCATGCAGATCGAGAACCGCAAGATCAAGCCCCAGAAGATCGAGATCGGGCATGCAGATCGAGATGAGATCGAGATCGAGATCGAGATCGAGATCGAGATCGAGATCGAGATCGAGATCGAGATCGAGATGATCAGATCGAGATCGAGATGATCGAGATGATCAGATCAGATCAGATGATCAGATC$ ${\tt AACCTGTTCAGCATCCTGCGCGGCGACAGCGACCTGAACAGCAAGCGCATGCTGACCCCCGAGGCCACCAAGGAGATCAAGCTGGTGGAGGAGAAGA}$ TCCAGAGCGCCCAGATCAACCGCATCGACCCCCTGGCCCCCTGCAGCTGCTGATCTTCGCCACCGCCCACAGCCCCACCGGCATCATCATCCAGAA

CACCGACCTGGTGGAGTGGAGCTTCCTGCCCCACAGCACCGTGAAGACCTTCACCCTGTACCTGGACCAGATCGCCACCCTGATCGGCCAGACCCGC CTGCGCATCATCAAGCTGTGCGGCAACGACCCCGACAAGATCGTGGTGCCCCTGACCAAGGAGCAGGTGCGCCAGGCCTTCATCAACAGCGGCGCCCT GGAAGATCGGCCTGGCCAACTTCGTGGGCATCATCGACAACCACTACCCCAAGACCAAGATCTTCCAGTTCCTGAAGCTGACCACCTGGATCCTGCC GTGATCAAGACCCCCTACCAGAGCGCCCAGCGCGCGAGCTGGTGGCCGTGATCACCGTGCTGCAGGACTTCGACCAGCCCATCAACATCATCAGCG CAACGCCCTGTGGCAGATGGACGTGACCCACGTGCCCAGCTTCGGCCGCCTGAGCTACGTGCACGTGACCGTGGACACCTACAGCCACTTCATCTGG GCCACCTGCCAGACCGGCGAGAGCACCAGCCACGTGAAGAAGCACCTGCTGAGCTGCTTCGCCGTGATGGGCCGTGCCCGAGAAGATCAAGACCGACA ACGGCCCCGGCTACTGCAGCAAGGCCTTCCAGAAGTTCCTGAGCCAGTGGAAGATCAGCCACCACCGGCATCCCCTACAACAGCCAGGGCCAGGC AACCTGGCCCTGTACACCCTGAACTTCCTGAACATCTACCGCAACCAGACCACCACCAGCGCGGGGAGCAGCACCTGACCGGCAAGAAGAACAGCCCCC ${\tt CCTGGACGACTGCATCAACGGCGGCAAGAGCCCCTACGCCTGCCGCAGCAGCTGCAGCGCTTAA}$

SEQ ID 67

 ${\tt MNPSEMQRKAPPRRRRRRRRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVSAGVPNSSEE$ TATIENGPA

SEQ ID 68

 ${\tt MNPSEMQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVYPTAPKRQR$ PSRTGHDDDGGFVEKKRGKCGEKQERSDCYCVCVERSRHRRLHFVLYA

SEQ ID 69

 ${\tt MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTLDLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQT$ EEDSVSVSDAPGSCIIDCNENTRKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSESKPRGTSPLPAGQVPVTLQ ${\tt GEGAQEGEPPTVEARYKSFSIKKLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAKSSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPV}$ NIDADQLLGIGQNWSTISQQALMQNEAIEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVIVELMAYENAN ${\tt PECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMHKAMLMAQAITGVVLGGQVRTFGRKCYNCGQIGHLKKNCPVLNKQNITIQATTTGREPPDLC}$

 $\tt MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTLDLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQT$ ${\tt EEDSVSVSDAPGSCIIDCNENTRKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSESKPRGTSPLPAGQVPVTLQ}$ GEGAQEGEPPTVEARYKSFSIKKLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAKSSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPV ${\tt NIDADQLLGIGQNWSTISQQALMQNEAIEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVIVELMAYENAN}$ PECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMHKAMLMAQAITGVVLGGQVRTFGRKCYNCGQIGHLKKNCPVLNKQNITIQATTTGREPPDLC

SEQ ID 71

 ${\tt MWATIVGKRAKGPASGPTTNWGIPNSAICSSGFSGTTTPTVPSVSGNKPVTTIQQLSPATSGSAAVDLCTIQAVSLLPGEPPQKTPTGVYGPLPKGT$ VGLILGRSSLNLKGVQIHTSVVDSDYKGEIQLVISSSIPWSASPRDRIAQLLLLPYIKGGNSEIKRIGGLGSTDPTGKAAYWASQVSENRPVCKAII $\tt QGKQFEGLVDTGADVSIIALNQWPKNWPKQKAVTGLVGIGTASEVYQSTEILHCLGPDNQESTVQPMITSIPLNLWGRDLLQQWGAEITMPAPSYSP$ TSQKIMTKMGYIPGKGLGKNEDGIKIPVEAKINQEREGIGNPC

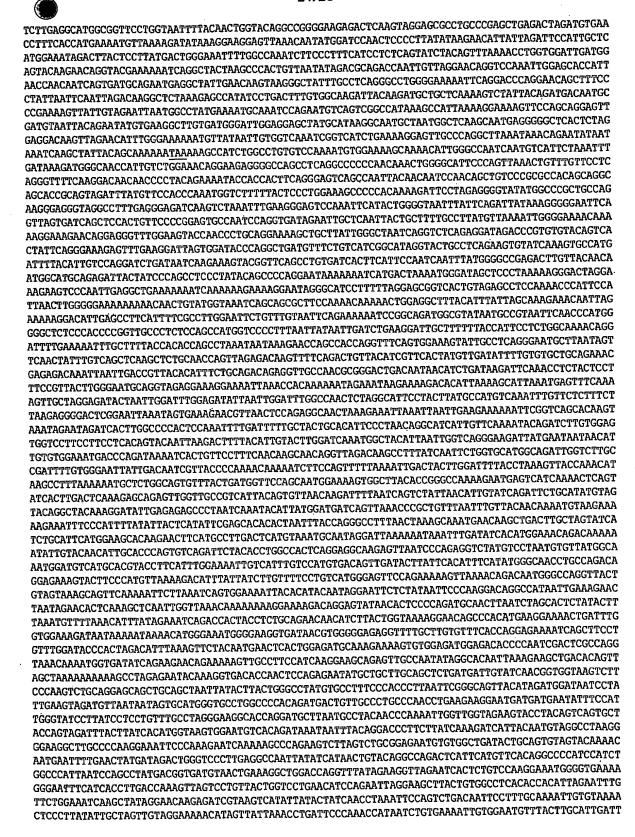
 ${\tt MWATIVGKRAKGPASGPTTNWGIPNSAICSSGFSGTTTPTVPSVSGNKPVTTIQQLSPATSGSAAVDLCTIQAVSLLPGEPPQKTPTGVYGPLPKGT$ VGLILGRSSLNLKGVQIHTSVVDSDYKGEIQLVISSSIPWSASPRDRIAQLLLLPYIKGGNSEIKRIGGLGSTDPTGKAAYWASQVSENRPVCKAII QGKQFEGLVDTGADVSIIALNQWPKNWPKQKAVTGLVGIGTASEVYQSTEILHCLGPDNQESTVQPMITSIPLNLWGRDLLQQWGAEITMPAPSYSP TSQKIMTKMGYIPGKGLGKNEDGIKIPVEAKINQEREGIGNPCA

SEQ ID 73

 ${\tt MNKSRKRRNRESLLGAATVEPPKPIPLTWKTEKPVWVNQWPLPKQKLEALHLLANEQLEKGHIEPSFSPWNSPVFVIQKKSGKWRMLTDLRAVNAVI$ ${\tt QPMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFYGRALQPVREKFSDCYII}$ ${\tt HCIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDTLKTLNDFQKLLGDINWIRPTLGIPTYAMS}$ NLFSILRGDSDLNSKRMLTPEATKEIKLVEEKIQSAQINRIDPLAPLQLLIFATAHSPTGIJIQNTDLVEWSFLPHSTVKTFTLYLDQIATLIGQTR LRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIFQFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKER ${\tt VIKTPYQSAQRAELVAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYITHIRAHTNLPGPLTKANEQA}\\$ DLLVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIVQHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIW NLALYTLNFLNIYRNQTTTSAEQHLTGKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPIRDAKKSTSAET ETSQSSTVDSQDEQNGDVRRTDEVAIHQEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCS

MNKSRKRRNRESLLGAATVEPPKPIPLTWKTEKPVWVNQWPLPKQKLEALHLLANEQLEKGHIEPSFSPWNSPVFVIQKKSGKWRMLTDLRAVNAVI QPMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYII HCIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDTLKTLNDFQKLLGDINWIRPTLGIPTYAMS ${\tt NLFSILRGDSDLNSKRMLTPEATKEIKLVEEKIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIATLIGQTR$ $\tt LRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIFQFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKER$ VIKTPYQSAQRAELVAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYITHIRAHTNLPGPLTKANEQA DLLVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIVQHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIW ${\tt ATCQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQGQAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQL}\\$ NLALYTINFLNIYRNQTTTSAEQHLTGKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPIRDAKKSTSAET ${\tt ETSQSSTVDSQDEQNGDVRRTDEVAIHQEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCSACCOMMONDATION CONTROL OF CONTRO$

TCTGCTTTGAGATGCTGTTAATCTGTAACCCTAGCCCCAACCCTGTGCTCACAGAAACAGGTGCTGTTGACTCAAGGTTTAATGGATTCAGGGCT GTGCAGGATGTGCTTTGTTAAACAAATGCTTGAAGGCAGCAAGCTTGTTAAGAGTCATCACCACTCCCTAATCTCAAGTAAGCAGGGACACAAACAC AGACCTGACTGTCCCCTGGCCCGACACCCGTAAAGGGTCTGTGCTGAGGATTAGTAAAAGAGGAAGGCAAGGCCTCTTTGCAGTTGAGATAAGAGGAAGCTGGAGGTGGGACATGCTGGCGGCAATACTGCTCTTTAAGGCATTGAGATGTTTATGTATATGCACATCAAAAGCACACCTTTTTTCTTTACCT TGTTTATGATGCAGAGACATTTGTTCACATGTTTTCCTGCTGGCCCTCTCCCCACTATTACCCTATTGTCCTGCCACATCCCCCTCTCCGAGATGGT A GAGATA A TGATCA A TAAA TACTGAGGGAACT CAGAGACC GGTGCGGCGGGGCCCCATATGCTGAGCGCCGGTCCCCTGGGCCCACTTTTCTTT $\tt GTGCCCAACGTGGATGCTTTTCTCTAGGGTGAAGGGACTCTCGAGTGTGGTCATTGAGGACAAGTCAACGAGAGATTCCCGAGTACGTCTACAGTGA$ TTTTCTCTGGGGACCCAGAGAGAAGGAGGCGTTTTCACCACAGCCGAACAGGGCAGGACCCCAGCACCCGGGACCCAGCGGACTTTGCCAAGGGGA TTTGAGCTGTACTAAGAAAAATTATTTTGCCTTGACCTGTTAACCTGTAACTGTAGCCCCAACCCTGTGCTCAAAGAAACATGTGCTGTATGGA ATCAAGGTTTAAGGGATCAAGGGCTGTACAGGATGTGCCTTGTTAACAATGTGTTTACAGGCAGTATGCTTGGTAAAAGTCATCGCCATTCTCCATT $\tt CTCCATTAATCAGGGGCACGATGCACTGCGGAAAGCCACAGGGACCTCTGCCCGAGAAAGCCTGGGTATTGTCCAAGGCTTCCCCCCACTGAGACAG$ GCCTCTTGCAGTTGAGATAAGAGGAAGGCCTCCGTCTCCTGCATGTCCTTGGGAATGGAATGTCTTGGTGTAAAACCCGATAGTACATTCCTTCTAT ${\tt TCTGAGAGAAAAACCACCCTGTGGCTGGAGGTGAGATATGCTAGCGGCAATGCTGCTCTGTTACTCTTTGCTACACTGAGATGTTTGGGTGGAGA}$ $\tt CTCCCCACTATCGCCCTGTTCTCCCACCGCATTCCCCTTGCTGAGATAGTGAAAATAGTAATCTGTAGATACCAAGGGAACTCAGAGACCATGGCCG$ GCTATTTCAAACAATAGAACAATTCTGCCCATGGTTTCCAGAACAGGGAACTTTAGATCTAAAAGATTGGGAAAAAATTGGCAAAGAATTAAAAACAA ${\tt GGTCCAGAATCATTGGGGCCATCAGAGCCTAAACCACGATCGCCATCAACTCCTCCTCCTGTGGTTCAGATGCCTGTAACATTACAACCTCAAACGC}$ ${\tt GCCGGTAGAAAATAAGACCCAACCGCTGGTAGTTTATCAATACCGGCTGCCAACCGAGCTTCAGTATCGGCCTCCTTCAGAGGTTCAATACAGACCT}$ CAAGCGGTGTGTCCTGTGCCAAATAGCACGGCACCATACCAGCAACCCACAGCGATGGCGTCTAATTCACCAGCAACACAGGACGCGGCGCTGTATC



TTTTTCAGTTACGATGTGACTGGAATACATCAGATTTTTGTGTTACACCACAAGCCTATAATGAGTCTGAGCATCACTGGGACATGGTTAGATGCCA TGGTGCCAGGAACGGAGACAATCGTGAAAGCTGCTGATAGCCTCACAAATCTTAAGCCAGTCACTTGGGTTAAAAGCATCAGAAGTTTCACTATTGT TAAGAAACTCCATTTTGATCTGTACTAAGAAAAATTGTTTTGCCTTGAGATGCTGTTAATCTGTAACTTTAGCCCCCAACCCTGTGCTCACGGAAACA TTCACATGTGTTTGAACAATATGAAATCAGTGCACCTTGAAAATGAACAGAATAACAGTGATTTTAGGGAACAAAGGAAGACAACCATAAGGTCTGA $\tt CTGCCTGAGGGGCCAAAAAGCCATATTTTCTTCTTGCAGAGAGCCTATAAATGGACGTGCAAGTAGGAGAGATATTGCTAAATTCTTTTCCT$ AGATAAGGACTGAGATACGCCCTGGTCTCCTGCAGTACCCTCAGGCTTACTAGGATTGGGAAACCCCAGTCCTGGTAAATTTGAGGTCAGGCCGGTT CTTTGCTCTGAACCCTGTTTTCTGTTAAGATGTTTATCAAGACAATACATGCACCGCTGAACATAGACCCTTATCAGGAGTTTCTGATTTTGCTCTG TTTTAAAATCCCTAATAAAAACTTGCTGGTTTTGTGGCTCAGGGGGGCATCATGGACCTACCAATACGTGATGTCACCCCCGGTGGCCCAGCTGTAA CACCCTGTGGCTGGAGGCGGGATATGCTGGCAGCAATGCTGCTCTATTACTCTTTGCTACACTGAGATGTTTGGGTGGAGAGAAGCATAAATCTGGC CACCTGATGAGAAATACCCACAGGTGTGGAGGGGCTGGCCCCCTTCA

GTTTCAGTTTCTGATGCCCCTAAAAGCTGTGTAACAGATTGTGAAGAAGAGGCAGGGACAGGAATCCCAGCAAGGAACGGAAAGTTCACATTGTAAAT ATGTAGCAGAGTCTGTAATGGCTCAGCCAAAATGTTGACTACAGTCAATTACAGGAGATAATATACCCTGAATCATCAAAATTTGGGGGAAGGAGGTCCAÇAATCATTGGGGCCATCAGAGCCTAAACCACGATCGCCATCAACTCCTCCTCCCGTGGTTCAGATGCCTGTAACATTACAACCTCAAACG CAGGTTAGACAAGCACAAACCCCAAGAGAAAATCAAGTAGAAAGGGACAGAGTCTCTATCCCGGCAATGCCAACTCAGATACAGTATCCACAATATC $ACC \verb|TTTCACCATGAAAATGTTAAAAGATATAAAGGAAGGAGTTAAACAATATGGATCCAACTCCCCTTATATAAGAACATTATTAGATTCCATTGCT$ GAGTACAAGAACAGGTACGAAAAAAATCAGGCTACTAAGCCCACTGTTAATATAGACGCAGACCAATTGTTAGGAACAGGTCCAAATTGGAGCACCAT TAACCAACAATCAGTGATGCAGAATGAGGCTATTGAACAAGTAAGGGCTATTTGCCTCAGGGCCTGGGGAAAAATTCAGGACCCAGGAACAGCTTTC CCTATTAATTCAATTAGACAAGGCTCTAAAGAGCCATATCCTGACTTTGTGGCAAGATTACAAGATGCTGCTCAAAAGTCTATTACAGATGACAATG ${\tt CCCGAAAAGTTATTGTAGAATTAATGGCCTATGAAAATGCAAATCCAGAATGTCAGTCGGCCATAAAGCCATTAAAAGGAAAAGTTCCAGCAGGAGT$ TGATGTAATTACAGAATATGTGAAGGCTTGTGATGGGATTGGAGGAGCTATGCATAAGGCAATGCTAATGGCTCAAGCAATGAGGGGGGCTCACTCTA CAGCACCGCAGTAA



CCCTGTTCCAGACCATCGAGCAGTTCTGCCCCTGGTTCCCCGAGCAGGGCACCCTGGACCTGAAGGACTGGGAGAAGATCGGCAAGGAGCTGAAGCA GGCCAACCGCGAGGGCAAGATCATCCCCCTGACCGTGTGGAACGACTGGGCCATCATCAAGGCCACCCTGGAGCCCTTCCAGACCGGCGAGGACATC AGCCCGTGGAGAACAAGACCCCAGCCCCTGGTGGTGTACCAGTACCGCCTGCCCACCGAGCTGCAGTACCGCCCCCCAGCGAGGTGCAGTACCGCCCCACGGCAACCGCCTGACCCCCTACGACTGGGAGATCCTGGCCAAGAGCAGCCTGAGCAGCCAGTACCTGCAGTTCAAGACCTGGTGGATCGACG GCGTGCAGGAGCAGGTGCGCAAGAACCAGGCCACCAAGCCCACCGTGAACATCGACGCCGACCAGCTGCTGGGCACCGGCCCCAACTGGAGCACCAT $\tt CCCGCAAGGTGATCGTGGAGCTGATGGCCTACGAGAACGCCAACCCCGAGTGCCAGAGCGCCATCAAGCCCCTGAAGGGCAAGGTGCCCGGCGT$ GGACGTGATCACCGAGTACGTGAAGGCCTGCGACGGCATCGGCGGCGCCATGCACAAGGCCATGCTGATGGCCCAGGCCATGCGCGGCCTGACCCTG TCAACCAGGCCATCACCGCCAAGAACAAGAAGCCCAGCGGCCTGTGCCCCAAGTGCGGCAAGGGCAAGCACTGGGCCAACCAGTGCCACAGCAAGTT CCGCCCCCAGGCTTAA

SEQ ID 78

MGQTESKYASYLSFIKILLRRGGVRASTENLITLFQTIEQFCPWFPEQGTLDLKDWEKIGKELKQANREGKIIPLTVWNDWAIIKATLEPFQTGEDI VSVSDAPKSCVTDCEEEAGTESQQGTESSHCKYVAESVMAQSTQNVDYSQLQEIIYPESSKLGEGGPESLGPSEPKPRSPSTPPPVVQMPVTLQPQT QVRQAQTPRENQVERDRVSIPAMPTQIQYPQYQPVENKTQPLVVYQYRLPTELQYRPPSEVQYRPQAVCPVPNSTAPYQQPTAMASNSPATQDAALY PQPPTVRLNPTASRSGQGGALHAVIDEARKQGDLEAWRFLVILQLVQAGEETQVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIA HGNRLTPYDWEILAKSSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEAIEQVRAICLRAWGKIQDPGTAF PINSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVIVELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQCHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVP QGFQGQQPLQKIPPLQGVSQLQQSNSCPAPQQAAPQ

SEQ ID 79

MGQTESKYASYLSFIKILLRRGGVRASTENLITLFQTIEQFCPWFPEQGTLDLKDWEKIGKELKQANREGKIIPLTVWNDWAIIKATLEPFQTGEDI
VSVSDAPKSCVTDCEEEAGTESQQGTESSHCKYVAESVMAQSTQNVDYSQLQEIIYPESSKLGEGGPESLGPSEPKPRSPSTPPPVVQMPVTLQPQT
QVRQAQTPRENQVERDRVSIPAMPTQIQYPQYQPVENKTQPLVVYQYRLPTELQYRPPSEVQYRPQAVCPVPNSTAPYQQPTAMASNSPATQDAALY
PQPPTVRLNPTASRSGQGGALHAVIDEARKQGDLEAWRFLVILQLVQAGEETQVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIA
HGNRLTPYDWEILAKSSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEAIEQVRAICLRAWGKIQDPGTAF
PINSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVIVELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQCHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVP
QGFQGQQPLQKIPPLQGVSQLQQSNSCPAPQQAAPQA

SEQ ID 80

 TGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAAATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCG GCAGAAGAAGATGCAGGCAGCTGAGTTGTTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCT ${\tt GAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAGTCACCGTCG}$ gaacctgatcaccctgttccagaccatcgagcagttctgcccctggttccccgagcagggcaccctggacctgaaggactgggagaagatcggcaag gagetgaagcaggecaaccgcgagggcaagatcatccccctgaccgtgtggaacgactgggccatcatcaaggccaccctggagcccttccagaccg gcgaggacatcgtgagcgtgagcgacgccccaagagctgcgtgaccgactgcgaggaggaggccggcaccgagagccagcagggcaccgagagcag cccccagtaccagcccgtggagaacaagacccagccctggtggtgtaccagtaccgcctgcccaccgagctgcagtaccgccccccagcgaggtgcagtaccgccccaggccgtgtgcccaacagcaccgcccctaccagcagcccaccgccatggccagcagcagcaacagcccgccaccaggacg ccgccctgtacccccagccccaccgtgcgcctgaaccccaccgccagccgcagcggccagggcggcgccctgcacgccgtgatcgacgaggcccg caagcagggcgacctggaggcctggcgcttcctggtgatcctgcagctggtgcaggccggcgaggagacccaggtgggcgccccgccgccgag acccgctgcgagcccttcaccatgaagatgctgaaggacatcaaggagggcgtgaagcagtacggcagcaacagcccctacatccgcaccctgctgg gtggatcgacggcgtgcaggagcaggtgcgcaagaaccaggccaccaagcccaccgtgaacatcgacgccgaccagctgctgggcaccggcccaac tggagcaccatcaaccagcagagcgtgatgcagaacgaggccatcgagcaggtgcgcccatctgcgcgcctggggcaagatccaggaccccg gcaccgccttccccatcaacagcatccgccagggcagcaaggagccctaccccgacttcgtggcccgcctgcaggacgcccagaagagcatcac cgacgacaacgcccgcaaggtgatcgtggagctgatggcctacgagaacgccaaccccgagtgccagagcgccatcaagcccctgaagggcaaggtg cccgccggcgtggacgtgatcaccgagtacgtgaaggcctgcgacggcatcggcggcgccatgcacaaggccatgctgatggcccaggccatgcgcggcctgaccctgggcggccaggtgcgcaccttcggcaagaagtgctacaactgcggccagatcggccacctgaagcgcagctgccccgtgctgaacaa gcagaacatcatcaaccaggccatcaccgccaagaacaagaagcccagcggcctgtgccccaagtgcggcaagggcaagcactgggccaaccagtgc CCCCCagcaggccgcccccaggcttaagaattcAGACTCGAGCAAGTCTAGAAAGCCATGGATATCGGATCCACTACGCGTTAGAGCTCGCTGATC TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAG ACAATAGCAGGGGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACC ${\tt TCGTCAAGAAGCCGATAGAAGCCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTT$ CAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCCAGCCGGCCACAGTCGATGAATCCAGAAAAAGCGGCCATTTTCCAC $\textbf{CGGCGGCATCAGAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGCCCCAAGCCGCCGAGAGCCTGCGAGAACCTGCGAGAACCTGCCAAGCCGCCAAGCCGCCGAGAGCCTGCCAATCCATCTTGCCCCAAGCCGCCCGAGAGCCTGCCGAATCCAATCCATCTTGCCCCAAGCCGCCGAGAGCCTGCCGAATCCAATCCATCTTGCCCCAAGCCGCCGAGAGCCTGCCGAATCCAATCCATCTTGCCCAAGCCGCCGAGAGAACCTGCCGAATCCAATCCATCTTGCCCAAGCCGCCGAGAGACCTGCCGAATCCAATCCATCTTGCCCGAATCCAATCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCAATCCAATCCAATCCAATCAATCCAATCAATCCAATCAATCCAATCAATCCAATCAA$ TTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCCATCAGATCCTTGGCGCGCAAGAAAGCCCATCCAGTTTACT TTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAA ATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGCCCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGA A CAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCGGATCAGCTTATGCGGTGTGAAATATATCAGCTCACAGGGGGTAATACGGTTATCCACAGAATCAGGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAA ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACC ${\tt CCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT}$ AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACTGAACGGTGATCCCCACCGGAATTGCG

SEQ ID 81

GTGTATGGGTACCTGGCCCCATAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATAAATATTTCCATTGGGTATCATTATCCTCC CACATGGTAAGCGGGATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTT GCCCCAAGGAAATTCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAAACAATGAATT CGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAGTCGTCCCAAGTGCACAAGTGAGTCCAGCTGTT GATAGCGACTTAACAGAAAGTTTAGACAAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCTTGGGAATGGGGAAAAAAGGAATCTCTACCCCAA ${\tt GACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCTTCACACCACATTAGAATTTGGTCTGGAAATCA}$ AACTTTAGAAACAAGAGATCGTAAGCCATTTTATACTATTGACCTGAATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATATG CTAGTTGTAGGAAATATAGTTATTAAACCAGACTCCCAGACTATAACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGC TGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATTGCAGTTAATTGCAGTCACAGCTACGGCTGCT GTAGCAGGAGTTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGATTGGCAAAAAAATTCTACAAGATTGTGGAATTCACAATCTAGTA ATGTGACTGGAATACGTCAGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGA GAAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAACAATTTTCGAAGCATCAAAAGCCCATTTAAATTTTGGTGCCAGGAACTGAGGCAATTG CAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAGACCATTGGAAGTACTACGATTATAAATCTCATATTAATCCTTGTGTG AAAAGAAAAGGGGGAAATGTGGGGAAAAGCAAGAGAGATCAGATTGTTACTGTGTCTGTGGCCTAA

SEQ ID 82

GCGAGGAGCAGATGAAGCTGCCCAGCACCAAGAAGGCCGAGCCCCCACCTGGGCCCAGCTGAAGAAGCTGACCCAGCTGGCCCACCAAGTACCTGGA GCGTGTGGGTGCCCGCCCATCGACGACCGCTGCCCCCCAAGCCCGAGGAGGAGGAGGAGGATGATCAACATCAGCATCGCTACCACTACCCCCC GCCCCAAGGAGATCCCCAAGGAGAGAGACACCGAGGTGCTGGTGTGGGAGGAGTGCGTGGCCAACAGCGCCGTGATCCTGCAGAACAACGAGTT $\tt CGGCACCATCATCGACTGGGCCCCCGCGGCCAGTTCTACCACAACTGCAGCGGCCAGACCCAGAGCTGCCCCAGCGCCCAGGTGAGCCCCGCCGTG$ GACAGCGACCTGACCGAGAGCCTGGACAAGCACAAGCACAAGAAGCTGCAGAGCTTCTACCCCTGGGAGTGGGGCGAGAAGGGCATCAGCACCCCCC $\tt CTGGTGGTGGGCAACATCGTGATCAAGCCCGACAGCCAGACCATCACCTGCGAGAACTGCCGCCTGCTGACCTGCATCGACAGCACCTTCAACTGGC$ AGCACCGCATCCTGCTGCGCGCCCCGCGAGGGCGTGTGGATCCCCGTGAGCATGGACCGCCCCTGGGAGGCCAGCCCCAGCGTGCACATCCTGAC TCGACCAGAAGCTGGCCAACCAGATCAACGACCTGCGCCAGACCGTGATCTGGATGGGCGACCGCTTGATGAGCCTGGAGCACCGCTTCCAGCTGCA GAGGACAACCTGACCCTGGACATCAGCAAGCTGAAGGAGCAGATCTTCGAGGCCAGCAAGGCCCACCTGAACCTGGTGCCCGGCACCGAGGCCATCG AAGCGCAAGGGCGGCAACGTGGGCAAGAGCAAGCGCGACCAGATCGTGACCGTGAGCGTGGCCTAA

SEQ ID 83

MNPSEMQRKAPPRRRHRNRAPLTHKMNKMVTSEEQMKLPSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAA
AANYTYWAYVPFPPLIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGYHYPPICLGRAPGCLMPAVQNWLVEVPTVSPICRFTY
HMVSGMSLRPRVNYLQDFSYQRSLKFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQSCPSAQVSPAV
DSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPELWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYM
LVVGNIVIKPDSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKGVLNRSKRFIFTLIAVIMGLIAVTATAA
VAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSIDQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRHLQGR
EDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTIINLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLS
KRKGGNVGKSKRDQIVTVSVA